

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
28 February 2002 (28.02.2002)

PCT

(10) International Publication Number
WO 02/16649 A2

(51) International Patent Classification⁷:

C12Q 1/68

(21) International Application Number:

PCT/US01/26519

(22) International Filing Date:

27 August 2001 (27.08.2001)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

60/227,948 25 August 2000 (25.08.2000) US
60/228,854 29 August 2000 (29.08.2000) US

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CR, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 02/16649 A2

(54) Title: PROBES AND DECODER OLIGONUCLEOTIDES

(57) Abstract: The present invention is directed to improved methods and compositions for the use of adapter sequences on arrays in a variety of multiplexed nucleic acid reactions, including synthesis reactions, amplification reactions, and genotyping reactions.

PROBES AND DECODER OLIGONUCLEOTIDES

This application claims the benefit of U.S.S.N.s 60/227,948 filed August 25, 2000 and 60/228,854, filed August 29, 2001, both of which are expressly incorporated herein by reference.

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FIELD OF THE INVENTION

The present invention is directed to methods and compositions for the use of adapter sequences on arrays in a variety of nucleic acid reactions, including synthesis reactions, amplification reactions, and 10 genotyping reactions.

BACKGROUND OF THE INVENTION

The detection of specific nucleic acids is an important tool for diagnostic medicine and molecular 15 biology research. Gene probe assays currently play roles in identifying infectious organisms such as bacteria and viruses, in probing the expression of normal and mutant genes and identifying mutant genes such as oncogenes, in typing tissue for compatibility preceding tissue transplantation, in matching tissue or blood samples for forensic medicine, and for exploring homology among genes from different species.

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Ideally, a gene probe assay should be sensitive, specific and easily automatable (for a review, see Nickerson, Current Opinion in Biotechnology 4:48-51 (1993)). The requirement for sensitivity (i.e. low detection limits) has been greatly alleviated by the development of the polymerase chain reaction (PCR) and other amplification technologies which allow researchers to amplify exponentially a specific 25 nucleic acid sequence before analysis (for a review, see Abramson et al., Current Opinion in Biotechnology, 4:41-47 (1993)).

Specificity, in contrast, remains a problem in many currently available gene probe assays. The extent of molecular complementarity between probe and target defines the specificity of the interaction. 30 Variations in the concentrations of probes, of targets and of salts in the hybridization medium, in the reaction temperature, and in the length of the probe may alter or influence the specificity of the

probe/target interaction.

It may be possible under some circumstances to distinguish targets with perfect complementarity from targets with mismatches, although this is generally very difficult using traditional technology, since

5 small variations in the reaction conditions will alter the hybridization. New experimental techniques for mismatch detection with standard probes include DNA ligation assays where single point mismatches prevent ligation and probe digestion assays in which mismatches create sites for probe cleavage.

Recent focus has been on the analysis of the relationship between genetic variation and phenotype by

10 making use of polymorphic DNA markers. Previous work utilized short tandem repeats (STRs) as polymorphic positional markers; however, recent focus is on the use of single nucleotide polymorphisms (SNPs), which occur at an average frequency of more than 1 per kilobase in human genomic DNA. Some SNPs, particularly those in and around coding sequences, are likely to be the

15 direct cause of therapeutically relevant phenotypic variants and/or disease predisposition. There are a number of well known polymorphisms that cause clinically important phenotypes; for example, the apoE2/3/4 variants are associated with different relative risk of Alzheimer's and other diseases (see Cordon et al., Science 261(1993)). Multiplex PCR amplification of SNP loci with subsequent

hybridization to oligonucleotide arrays has been shown to be an accurate and reliable method of simultaneously genotyping at least hundreds of SNPs; see Wang et al., Science, 280:1077 (1998);

20 see also Schafer et al., Nature Biotechnology 16:33-39 (1998). The compositions of the present invention may easily be substituted for the arrays of the prior art.

There are a variety of particular techniques that are used to detect sequence, including mutations and SNPs. These include, but are not limited to, ligation based assays, cleavage based assays (mismatch

25 and invasive cleavage such as Invader™), single base extension methods (see WO 92/15712, EP 0 371 437 B1, EP 0317 074 B1; Pastinen et al., Genome Res. 7:606-614 (1997); Syvänen, Clinica Chimica Acta 226:225-236 (1994); and WO 91/13075), and competitive probe analysis (e.g. competitive sequencing by hybridization; see below).

30 Oligonucleotide ligation amplification ("OLA", which is referred as the ligation chain reaction (LCR) when two-stranded reactions or nested reactions are done) involves the ligation of two smaller probes into a single long probe, using the target sequence as the template. See generally U.S. Patent Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; WO 97/31256 and WO 89/09835, all of which are incorporated by reference.

35 Invasive cleavage technology is based on structure-specific nucleases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently hybridize to a target sequence with a non-complementary overlap. The enzyme cleaves at the overlap due to its recognition of the "tail", and releases the "tail" with a label. This can then be

detected. The Invader™ technology is described in U.S. Patent Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; and 5,843,669, all of which are hereby incorporated by reference.

An additional technique utilizes sequencing by hybridization. For example, sequencing by hybridization has been described (Drmanac et al., *Genomics* 4:114 (1989); Koster et al., *Nature Biotechnology* 14:1123 (1996); U.S. Patent Nos. 5,525,464; 5,202,231 and 5,695,940, among others, all of which are hereby expressly incorporated by reference in their entirety).

Sensitivity, i.e. detection limits, remain a significant obstacle in nucleic acid detection systems, and a variety of techniques have been developed to address this issue. Briefly, these techniques can be classified as either target amplification or signal amplification. Target amplification involves the amplification (i.e. replication) of the target sequence to be detected, resulting in a significant increase in the number of target molecules. Target amplification strategies include the polymerase chain reaction (PCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA).

Alternatively, rather than amplify the target, alternate techniques use the target as a template to replicate a signalling probe, allowing a small number of target molecules to result in a large number of signalling probes, that then can be detected. Signal amplification strategies include the ligase chain reaction (LCR), cycling probe technology (CPT), invasive cleavage techniques such as Invader™ technology, Q-Beta replicase (QβR) technology, and the use of "amplification probes" such as "branched DNA" that result in multiple label probes binding to a single target sequence.

The polymerase chain reaction (PCR) is widely used and described, and involves the use of primer extension combined with thermal cycling to amplify a target sequence; see U.S. Patent Nos. 4,683,195 and 4,683,202, and PCR Essential Data, J. W. Wiley & sons, Ed. C.R. Newton, 1995, all of which are incorporated by reference. In addition, there are a number of variations of PCR which also find use in the invention, including "quantitative competitive PCR" or "QC-PCR", "arbitrarily primed PCR" or "AP-PCR", "immuno-PCR", "Alu-PCR", "PCR single strand conformational polymorphism" or "PCR-SSCP", allelic PCR (see Newton et al. *Nucl. Acid Res.* 17:2503 91989); "reverse transcriptase PCR" or "RT-PCR", "biotin capture PCR", "vectorette PCR", "panhandle PCR", and "PCR select cDNA subtraction", among others.

Strand displacement amplification (SDA) is generally described in Walker et al., in Molecular Methods for Virus Detection, Academic Press, Inc., 1995, and U.S. Patent Nos. 5,455,166 and 5,130,238, all of which are hereby incorporated by reference.

Nucleic acid sequence based amplification (NASBA) is generally described in U.S. Patent No. 5,409,818 and "Profiting from Gene-based Diagnostics", CTB International Publishing Inc., N.J., 1996,

both of which are incorporated by reference.

Cycling probe technology (CPT) is a nucleic acid detection system based on signal or probe amplification rather than target amplification, such as is done in polymerase chain reactions (PCR).

5 Cycling probe technology relies on a molar excess of labeled probe which contains a scissile linkage of RNA. Upon hybridization of the probe to the target, the resulting hybrid contains a portion of RNA:DNA. This area of RNA:DNA duplex is recognized by RNaseH and the RNA is excised, resulting in cleavage of the probe. The probe now consists of two smaller sequences which may be released, thus leaving the target intact for repeated rounds of the reaction. The unreacted probe is removed and
10 the label is then detected. CPT is generally described in U.S. Patent Nos. 5,011,769, 5,403,711, 5,660,988, and 4,876,187, and PCT published applications WO 95/05480, WO 95/1416, and WO 95/00667, all of which are specifically incorporated herein by reference.

15 The oligonucleotide ligation assay (OLA) involve the ligation of at least two smaller probes into a single long probe, using the target sequence as the template for the ligase. See generally U.S. Patent Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; and WO 89/09835, all of which are incorporated by reference.

20 Invader™ technology is based on structure-specific polymerases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently hybridize to a target sequence with overlap. For mismatch discrimination, the invader technology relies on complementarity at the overlap position where cleavage occurs. The enzyme cleaves at the overlap, and releases the "tail" which may or may not be labeled. This can then be detected. The Invader™ technology is described in U.S. Patent Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; 25 and 5,843,689, all of which are hereby incorporated by reference.

30 "Branched DNA" signal amplification relies on the synthesis of branched nucleic acids, containing a multiplicity of nucleic acid "arms" that function to increase the amount of label that can be put onto one probe. This technology is generally described in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference.

35 Similarly, dendrimers of nucleic acids serve to vastly increase the amount of label that can be added to a single molecule, using a similar idea but different compositions. This technology is as described in U.S. Patent No. 5,175,270 and Nilsen et al., J. Theor. Biol. 187:273 (1997), both of which are incorporated herein by reference.

U.S.S.N.s 09/189,543; 08/944,850; 09/033,462; 09/287,573; 09/151,877; 09/187,289 and 09/256,943; and PCT applications US98/09163 and US99/14387; US98/21193; US99/04473 and US98/05025, all

of which are expressly incorporated by reference, describe novel compositions utilizing substrates with microsphere arrays, which allow for novel detection methods of nucleic acid hybridization.

The use of adapter-type sequences that allow the use of universal arrays has been described in limited contexts; see for example Chee et al., Nucl. Acid Res. 19:3301 (1991); Shoemaker et al., Nature Genetics 14:450 (1996); U.S. Patent Nos. 5,494,810, 5,830,711, 6,027,889, 6,054,564, and 6,268,148; and EP 0 799 897 A1; WO 97/31256, all of which are expressly incorporated by reference.

Accordingly, it is an object of the present invention to provide methods for detecting nucleic acid reactions, and other target analytes, on arrays using adapter sequences.

SUMMARY OF THE INVENTION

In accordance with the above objects, the invention also provides a method of detecting a target nucleic acid. The method comprises contacting the target nucleic acid with an adapter sequence such that the target nucleic acid is joined to the adapter sequence to form a modified target nucleic acid. In addition, the method comprises contacting the modified target nucleic acid with an array comprising a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified target nucleic acid form a complex, wherein the microspheres are distributed on the surface, and detecting the presence of the target nucleic acid. In addition the method comprises adding at least one decoding binding ligand to the array such that the identity of the target nucleic acid is determined. Preferably the adapter nucleic acids include a sequence as set forth in Table I, Table II, Table III or Table IV.

In addition the invention provides a method of making an array. The method comprises forming a surface comprising individual sites on a substrate, distributing microspheres on the surface such that the individual sites contain microspheres, wherein the microspheres comprise at least a first and a second subpopulation each comprising a capture probe, wherein the capture probe is complementary to an adapter sequence, the adapter sequence joined to a target nucleic acid, and an identifier binding ligand that will bind at least one decoder binding ligand such that the identification of the target nucleic acid is elucidated. Preferably the adapter nucleic acids include a sequence as set forth in Table I, Table II, Table III or Table IV.

In addition the invention provides a kit comprising at least one nucleic acid selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV. In one embodiment the invention provides a kit that includes a nucleic acid that includes a sequence as set forth in Table I, Table II, Table III or Table IV and at least a first universal priming sequence.

In addition the invention includes an array composition comprising a first population of microspheres comprising first and second subpopulations, wherein the first subpopulation includes a first nucleic acid selected from the sequences set forth in Table I, Table II, Table III or Table IV and the second subpopulation includes a second sequence selected from the sequences set forth in Table I, Table II, 5 Table III or Table IV.

In addition the invention includes an array composition comprising a first sequence at a known location on a substrate, wherein the first sequence is selected from the sequences set forth in Table I, Table II, Table III or Table IV.

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In addition the invention includes a method for making an array. The method includes distributing a population of microspheres on an substrate, wherein the population includes first and second subpopulations, wherein the first subpopulation includes a first sequence selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV and the second

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subpopulation includes a second sequence selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV.

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In addition the method includes a method of immobilizing a target nucleic acid. The method includes hybridizing a first adapter probe with a first target nucleic acid, wherein the first adapter probe comprises a first domain that is complementary to the first target nucleic acid and a second domain, comprising a first sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV to form a first hybridization complex. In addition the method includes contacting the first hybridization complex with a first capture probe immobilized on a first substrate, wherein the first capture probe is substantially complementary to the second domain of the first adapter probe.

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In addition the invention includes a method of decoding an array composition comprising providing an array composition that includes a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent. The microspheres are distributed on the surface. The method further includes adding a plurality of decoding binding ligands to the array composition to identify the location of at least a plurality of the bioactive agents wherein at least a first decoder binding ligand comprises a sequence selected from the group consisting of the sequences of Table I, Table II, Table III or Table IV.

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A method of detecting a target nucleic acid sequence, said method comprising attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein the first adapter nucleic acid includes a sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV. The method further includes contacting the modified first target nucleic acid sequence with an array comprising a substrate with a patterned surface

comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified first target nucleic acid sequence form a hybridization complex; wherein the microspheres are distributed on the surface and detecting the presence of the modified first target nucleic acid sequence.

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DETAILED DESCRIPTION OF THE FIGURES

Figure 1 depicts a method of selecting oligonucleotide sequences.

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Figure 2 depicts a scheme for selection of probes and decoder oligonucleotides.

Figure 3 demonstrates hybridization intensity comparison of immobilized beads using non-purified oligonucleotides with HPLC purified oligonucleotides.

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Figure 4 depicts different oligonucleotide sequences immobilized onto silica beads at various salt concentration. Average intensity indicates hybridization intensity of beads in a BeadArray.

Figure 5 depicts immobilization of oligonucleotides in increasing salt concentrations.

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DETAILED DESCRIPTION OF THE INVENTION

This invention is directed to the use of adapter sequences, and optionally capture extender probes, that allow the use of "universal" arrays. That is, a "universal" array is an array with a set of capture probes that will hybridize to adapter sequences, for use in any number of different reactions, including the binding of nucleic acid reactions and other target analytes comprising a nucleic acid adapter sequence that can hybridize to the array. In this way, a manufacturer of arrays can make one type of array that may be used in a variety of applications, thus reducing the manufacturing costs associated with the array. In addition, in the case of bead arrays, the decoding steps as outlined below can be simplified, as one set of decoding probes can be made.

In general, the use of adapter sequences can be described as follows for nucleic acid reactions. An adapter sequence can be added exogenously to a target nucleic acid sequence using any number of different techniques, including, but not limited to, amplification reactions as described in U.S.S.N.

35 09/425,633, filed October 22, 1999; 09/513,362, filed February 25, 2000; 09/517,945, filed March 3, 2000; 09/535,854, filed March 27, 2000; 09/553,993, filed April 20, 2000; 09/556,463, filed April 21, 2000; 60/135,051, filed May 20, 1999; 60/135,053, filed May 20, 1999; 60/135,123, filed May 20, 1999; 60/130,089, filed April 20, 1999; 60/160,917, filed October 22, 1999; 60/160,927, filed October 22,

1999; 60/161,148, filed October 22, 1999; and 60/244,119, filed October 26, 2000 all of which are hereby incorporated by reference. In addition, the adapter can be added to an extension probe. The adapter sequence can then be used to target to its complementary capture probe on the surface.

- 5 Alternatively, the adapter sequences can be added to other target analytes, to generate unique and reproducible arrays of target analytes in a similar manner. By adding the nucleic acid to the target analyte (for example to an antibody in an immunoassay), the target analytes may then be arrayed.

Accordingly, the present invention provides methods for the detection of target analytes, particularly 10 nucleic acid target sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and 15 soil samples); biological warfare agent samples; research samples; purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.; As will be appreciated by those in the art, virtually any experimental manipulation may have been done on the sample.

20 The present invention provides methods for the detection of target analytes, particularly nucleic acid target sequences, in a sample. By "target analyte" or "analyte" or grammatical equivalents herein is meant any molecule, compound or particle to be detected. As outlined below, target analytes preferably bind to binding ligands, as is more fully described below. As will be appreciated by those in the art, a large number of analytes may be detected using the present methods; basically, any target 25 analyte for which a binding ligand, described below, may be made may be detected using the methods of the invention.

Suitable analytes include organic and inorganic molecules, including biomolecules. In a preferred embodiment, the analyte may be an environmental pollutant (including pesticides, insecticides, toxins, 30 etc.); a chemical (including solvents, polymers, organic materials, etc.); therapeutic molecules (including therapeutic and abused drugs, antibiotics, etc.); biomolecules (including hormones, cytokines, proteins, lipids, carbohydrates, cellular membrane antigens and receptors (neural, hormonal, nutrient, and cell surface receptors) or their ligands, etc); whole cells (including prokaryotic (such as pathogenic bacteria) and eukaryotic cells, including mammalian tumor cells); viruses 35 (including retroviruses, herpesviruses, adenoviruses, lentiviruses, etc.); and spores; etc. Particularly preferred analytes are environmental pollutants; nucleic acids; proteins (including enzymes, antibodies, antigens, growth factors, cytokines, etc); therapeutic and abused drugs; cells; and viruses.

In a preferred embodiment, the target analyte is a protein. As will be appreciated by those in the art,

there are a large number of possible proteinaceous target analytes that may be detected using the present invention. By "proteins" or grammatical equivalents herein is meant proteins, oligopeptides and peptides, derivatives and analogs, including proteins containing non-naturally occurring amino acids and amino acid analogs, and peptidomimetic structures. The side chains may be in either the 5 (R) or the (S) configuration. In a preferred embodiment, the amino acids are in the (S) or L-configuration. As discussed below, when the protein is used as a binding ligand, it may be desirable to utilize protein analogs to retard degradation by sample contaminants.

Suitable protein target analytes include, but are not limited to, (1) immunoglobulins, particularly IgEs, 10 IgGs and IgMs, and particularly therapeutically or diagnostically relevant antibodies, including but not limited to, for example, antibodies to human albumin, apolipoproteins (including apolipoprotein E), human chorionic gonadotropin, cortisol, α -fetoprotein, thyroxin, thyroid stimulating hormone (TSH), antithrombin, antibodies to pharmaceuticals (including antiepileptic drugs (phenytoin, primidone, carbamazepine, ethosuximide, valproic acid, and phenobarbital); cardioactive drugs (digoxin, lidocaine, procainamide, and disopyramide), bronchodilators (theophylline), antibiotics (chloramphenicol, sulfonamides), antidepressants, immunosuppressants, abused drugs (amphetamine, methamphetamine, cannabinoids, cocaine and opiates) and antibodies to any number of viruses (including orthomyxoviruses, (e.g. influenza virus), paramyxoviruses (e.g respiratory syncytial virus, mumps virus, measles virus), adenoviruses, rhinoviruses, coronaviruses, reoviruses, togaviruses (e.g. rubella virus), parvoviruses, poxviruses (e.g. variola virus, vaccinia virus), enteroviruses (e.g. poliovirus, coxsackievirus), hepatitis viruses (including A, B and C), herpesviruses (e.g. Herpes simplex virus, varicella-zoster virus, cytomegalovirus, Epstein-Barr virus), rotaviruses, Norwalk viruses, hantavirus, arenavirus, rhabdovirus (e.g. rabies virus), retroviruses (including HIV, HTLV-I and -II), papovaviruses (e.g. papillomavirus), polyomaviruses, and picornaviruses, and the like), and 15 bacteria (including a wide variety of pathogenic and non-pathogenic prokaryotes of interest including *Bacillus*; *Vibrio*, e.g. *V. cholerae*; *Escherichia*, e.g. Enterotoxigenic *E. coli*, *Shigella*, e.g. *S. dysenteriae*; *Salmonella*, e.g. *S. typhi*; *Mycobacterium* e.g. *M. tuberculosis*, *M. leprae*; *Clostridium*, e.g. *C. botulinum*, *C. tetani*, *C. difficile*, *C. perfringens*; *Corynebacterium*, e.g. *C. diphtheriae*; *Streptococcus*, *S. pyogenes*, *S. pneumoniae*; *Staphylococcus*, e.g. *S. aureus*; *Haemophilus*, e.g. *H. influenzae*; 20 *Neisseria*, e.g. *N. meningitidis*, *N. gonorrhoeae*; *Yersinia*, e.g. *G. lamblia*; *Y. pestis*, *Pseudomonas*, e.g. *P. aeruginosa*, *P. putida*; *Chlamydia*, e.g. *C. trachomatis*; *Bordetella*, e.g. *B. pertussis*; *Treponema*, e.g. *T. palladium*; and the like); (2) enzymes (and other proteins), including but not limited to, enzymes used as indicators of or treatment for heart disease, including creatine kinase, lactate dehydrogenase, aspartate amino transferase, troponin T, myoglobin, fibrinogen, cholesterol, triglycerides, thrombin, 25 tissue plasminogen activator (tPA); pancreatic disease indicators including amylase, lipase, chymotrypsin and trypsin; liver function enzymes and proteins including cholinesterase, bilirubin, and alkaline phosphatase; aldolase, prostatic acid phosphatase, terminal deoxynucleotidyl transferase, and bacterial and viral enzymes such as HIV protease; (3) hormones and cytokines (many of which serve 30 as ligands for cellular receptors) such as erythropoietin (EPO), thrombopoietin (TPO), the interleukins

(including IL-1 through IL-17), insulin, insulin-like growth factors (including IGF-1 and -2), epidermal growth factor (EGF), transforming growth factors (including TGF- α and TGF- β), human growth hormone, transferrin, epidermal growth factor (EGF), low density lipoprotein, high density lipoprotein, leptin, VEGF, PDGF, ciliary neurotrophic factor, prolactin, adrenocorticotrophic hormone (ACTH), calcitonin, human chorionic gonadotropin, cortisol, estradiol, follicle stimulating hormone (FSH), thyroid-stimulating hormone (TSH), luteinizing hormone (LH), progesterone, testosterone, ; and (4) other proteins (including α -fetoprotein, carcinoembryonic antigen CEA).

In addition, any of the biomolecules for which antibodies may be detected may be detected directly as

well; that is, detection of virus or bacterial cells, therapeutic and abused drugs, etc., may be done directly.

Suitable target analytes include carbohydrates, including but not limited to, markers for breast cancer (CA15-3, CA 549, CA 27.29), mucin-like carcinoma associated antigen (MCA), ovarian cancer (CA125), pancreatic cancer (DE-PAN-2), and colorectal and pancreatic cancer (CA 19, CA 50, CA242).

In a preferred embodiment, the target analyte (and various adapters and other probes of the invention), comprise nucleic acids. By "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramide (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al., Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 91986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Bru et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S.

Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within the definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done to facilitate the addition of labels, alter the hybridization properties of the nucleic acids, or to increase the stability and half-life of such molecules in physiological environments.

10 As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made. Alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

15 Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit 20 a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. This allows for better detection of mismatches. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration.

25 The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthanine hypoxanthanine, isocytosine, isoguanine, etc. A preferred embodiment utilizes isocytosine and isoguanine in nucleic acids designed to be complementary to other probes, rather than 30 target sequences, as this reduces non-specific hybridization, as is generally described in U.S. Patent No. 5,681,702. As used herein, the term "nucleoside" includes nucleotides as well as nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

35 In general, probes of the present invention (including adapter sequences and capture probes, described below) are designed to be complementary to a target sequence (either the target sequence of the sample or to other probe sequences, for example adapter sequences) such that hybridization of the target and the probes of the present invention occurs. This complementarity need not be perfect;

there may be any number of base pair mismatches that will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by

5 "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under the selected reaction conditions.

When nucleic acids are to be detected, they are referred to herein as "target nucleic acids" or "target sequences". The term "target sequence" or "target nucleic acid" or grammatical equivalents herein

10 means a nucleic acid sequence on a single strand of nucleic acid. The target sequence may be a portion of a gene, a regulatory sequence, genomic DNA, cDNA, RNA including mRNA and rRNA, or others. As is outlined herein, the target sequence may be a target sequence from a sample, or a derivative target such as a product of a reaction such as a detection sequence from an Invader™

15 reaction, a ligated probe from an OLA reaction, an extended probe from an SBE reaction, etc. It may be any length, with the understanding that longer sequences are more specific. As will be appreciated by those in the art, the complementary target sequence may take many forms. For example, it may be contained within a larger nucleic acid sequence, i.e. all or part of a gene or mRNA, a restriction

20 fragment of a plasmid or genomic DNA, among others. As is outlined more fully below, probes are made to hybridize to target sequences to determine the presence or absence of the target sequence in a sample. Generally speaking, this term will be understood by those skilled in the art. The target

25 sequence may also be comprised of different target domains; for example, a first target domain of the sample target sequence may hybridize to a capture probe, a second target domain may hybridize to a portion of a label probe, etc. The target domains may be adjacent or separated as indicated. Unless specified, the terms "first" and "second" are not meant to confer an orientation of the sequences with respect to the 5'-3' orientation of the target sequence. For example, assuming a 5'-3' orientation of the complementary target sequence, the first target domain may be located either 5' to the second domain, or 3' to the second domain. In addition, as will be appreciated by those in the art, the probes on the surface of the array (e.g. attached to the microspheres) may be attached in either orientation, either such that they have a free 3' end or a free 5' end.

30 As is more fully outlined below, the target sequence may comprise a position for which sequence information is desired, generally referred to herein as the "detection position" or "detection locus". In a preferred embodiment, the detection position is a single nucleotide, although in some embodiments, it may comprise a plurality of nucleotides, either contiguous with each other or separated by one or more nucleotides. By "plurality" as used herein is meant at least two. As used herein, the base which basepairs with a detection position base in a hybrid is termed a "readout position" or an "interrogation position".

In some embodiments, as is outlined herein, the target sequence may not be the sample target

sequence but instead is a product of a reaction herein, sometimes referred to herein as a "secondary" or "derivative" target sequence. Thus, for example, in SBE, the extended primer may serve as the target sequence; similarly, in invasive cleavage variations, the cleaved detection sequence may serve as the target sequence.

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If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification as needed, as will be appreciated by those in the art.

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Once prepared, the target sequence can be used in a variety of reactions for a variety of reasons. For example, in a preferred embodiment, genotyping reactions are done. Similarly, these reactions can also be used to detect the presence or absence of a target sequence. Sequencing or amplification reactions are also preferred. In addition, in any reaction, quantitation of the amount of a target sequence may be done.

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Furthermore, as outlined below for each reaction, many of these techniques may be used in a solution based assay, wherein the reaction is done in solution and a reaction product is bound to the array for subsequent detection, or in solid phase assays, where the reaction occurs on the surface and is detected.

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In general, the present invention provides pairs of capture probes (nucleic acids that are attached to addresses on arrays) and adapter sequences (sequences that are either perfectly or substantially complementary to the capture probe sequences) that can be used in a wide variety of ways, to immobilize target nucleic acids (either primary targets, such as genomic DNA, mRNA or cDNA, or

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secondary targets such as amplicons from a nucleic acid amplification or extension reaction, as outlined herein) to the addresses of the array. Thus, all the sequences in the Tables include their complements, and either sequence can be used as a capture probe (e.g. spotted onto a surface or attached to a microsphere of an array) or as the adapter sequence that binds to the capture probe.

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Accordingly, by "adapter sequences" or "adapters" or grammatical equivalents is meant a nucleic acid segment generally non-native or exogenous to a target molecule that is used to immobilize the target molecule to a solid support via binding to a capture probe sequence. In a preferred embodiment the adapter sequences and capture probes are selected from the sequences set forth in Table I, Table II, Table III or Table IV.

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Table I includes the sequence of the preferred 4000 sequences labeled "Decoder (5'-3')", and inherent in this table are the complementary sequences as well. In addition, the invention includes oligonucleotides that are complementary to those depicted in Table 1.

Table II includes the sequence of the preferred adapter/capture probe sequences and their complementary sequence. Table 2 depicts a preferred subset of 3172 decoder oligonucleotides and their complementary probe oligonucleotides. Accordingly, the invention provides compositions comprising a sequence as outlined in Table 2. In addition, the invention provides a composition comprising a complementary binding pair as outlined in Table 2.

Table 3 includes a preferred subset of 768 decoder oligonucleotides and complementary probe sequences. In some embodiments it may be desirable to include a uniform base at a terminus of the oligonucleotide, such as a T at the 5' end as depicted in Table 4. The inclusion of this uniform or constant base facilitates uniform labeling of the oligonucleotides.

These sequences are used as decoder probes, capture probes or adapter sequences as outlined in U.S.S.N. 09/344,526 and PCT/US99/14387, and U.S.S.N.s 60/160,917 and 09/5656,463 all of which are expressly incorporated by reference in their entirety.

As will be appreciated by those in the art, the length of the capture probe/adapter sequences will vary, depending on the desired "strength" of binding and the number of different adapters desired. In a preferred embodiment, adapter sequences range from about 5 to about 500 basepairs in length, with from about 8 to about 100 being preferred, and from about 10 to about 50 being particularly preferred.

As will be appreciated by those in the art, it is desirable to have adapter sequences that do not have significant homology to naturally occurring target sequences, to avoid non-specific or erroneous binding of target sequences to the capture probes. Accordingly, preferred embodiments utilize some method to select useful adapter sequences. In a preferred embodiment the method is outlined in Figure 1. Briefly, random 24-mer (or could be any desired length as outlined herein), sequences were assembled and subjected to certain defined screening procedures including such steps as requiring that the Tm of each of the sequence be within a pre-defined range. In addition the GC content must be balanced with the AT content and the self-complementarity must be minimized. In addition GC runs should be minimized, that is, runs of Gs or Cs should be reduced. In addition, decoder (adapter) to decoder (adapter) complementarity should be reduced so that the adapters do not hybridize with each other. Finally, the sequences are screened against a specified genomic database. In a preferred embodiment the adapters comprise at least one sequence selected from the sequences in Table I, Table II, Table III or Table IV.

In a preferred embodiment, the adapter sequences are chosen on the basis of a decoding step. As is more fully outlined below, a decoding step is used to decode random bead arrays. In this embodiment, a set of candidate capture probes is chosen; this may be done in a variety of ways. In a preferred embodiment, the sequences are generated randomly, each of a sufficient length to ensure a

low probability of occurring naturally. In some embodiments, for example when the array will be used with a particular organism's genome (e.g. the human genome, the *Drosophila* genome, etc.), the sequences are compared to the genome as a first filter, for example to remove sequences that would cross hybridize. Additionally, further filtering may be done using well-known methods, such as known methods for selecting good PCR primers. These techniques generally include steps that remove sequences that may have a propensity to form secondary structures or otherwise to cross-hybridize. Additionally, sequences that have extremes of melting temperatures can be optionally discarded, depending on the planned assay conditions.

- 5 Once a set of candidate capture probes is obtained, an array comprising the capture probes is made, and a matching set of decoding probes comprising the adapter sequences (e.g. the complements of the capture probes), as more fully outlined below, is made. Decoding then proceeds. Probes that do not hybridize well, for whatever reason, will not decode well, generally due to weak signals, and are generally discarded. Probes that cross-hybridize will also not decode well, as they will give ambiguous or mixed decoding signals. Only probes that hybridize sufficiently strongly and specifically will decode.
- 10 Thus, by setting suitable thresholds for signal strength and signal purity, adapter sequences that perform according to specified criteria are identified. Additionally, by setting a range on signal strength, capture probe/adapter sequence pairs that perform similarly (but hybridize specifically) are identified. In a preferred embodiment, decoding reactions are repeated, under a variety of conditions,
- 15 20 to test the robustness of the sequence pair.

Once identified, the adapter sequences are added to target sequences in a variety of ways, as will be appreciated by those in the art. In a preferred embodiment, nucleic acid amplification reactions are done, as is generally outlined in "Detection of Nucleic Acid Amplification Reactions Using Bead Arrays" and "Sequence Determination of Nucleic Acids using Arrays with Microspheres", both of which were filed on October 22, 1999, (U.S.S.N.'s 60/161,148 and 09/425,633, respectively), both of which are hereby incorporated by reference in their entirety. These may be either target amplification or signal amplification. In general, the techniques can be described as follows. Most amplification techniques require one or more primers hybridizing to all or part the target sequence (e.g. that hybridize to a target domain). The adapter sequences can be added to one or more of the primers (depending on the configuration/orientation of the system and need) and the amplification reactions are run. Thus, for example, PCR primers comprising at least one adapter sequence (and preferably one on each PCR primer) may be used; one or both of the ligation probes of an OLA or LCR reaction may comprise an adapter sequence; the sequencing primers for pyrosequencing, single-base extension, reversible chain termination, etc., reactions may comprise an adapter sequence; either the invader probe or the signalling probe of invasive cleavage reactions can comprise an adapter sequence; etc. Similarly, for signal detection techniques, the probes may comprise adapter sequences, with preferred methods utilizing removal of the unreacted probes. In addition, primers may include universal priming sequences. That is, the adapters may additionally contain universal priming sequences for universal

amplification of products of any of the reactions described herein. Universal priming sequences are further outlined in 09/779376, filed February 7, 2001; 09/779202, filed February 7, 2001; 09/915231, filed July 24, 2001; 60/180810, filed February 7, 2000; and 60/297609, filed June 11, 2001; and 60/311194 filed August 9, 2001, all of which are expressly incorporated herein by reference.

- 5 In an alternative embodiment, non-nucleic acid reactions are used to add adapter sequences to the nucleic acid targets. For example, for the direct detection of non-amplified target sequences (e.g. genomic DNA samples, etc.) on universal arrays, non-amplification methods are required. In this embodiment, binding partner pairs or chemical methods may be used. For example, one member of a
10 binding partner pair may be attached to the adapter sequence and the other member attached to the target sequence. For example, the binding partner be a hapten or antigen, which will bind its binding partner. For example, suitable binding partner pairs include, but are not limited to: antigens (such as proteins (including peptides)) and antibodies (including fragments thereof (FAbs, etc.)); proteins and small molecules, including biotin/streptavidin and digoxigenin and antibodies; enzymes and substrates
15 or inhibitors; other protein-protein interacting pairs; receptor-ligands; and carbohydrates and their binding partners, are also suitable binding pairs. Nucleic acid - nucleic acid binding proteins pairs are also useful. In general, the smaller of the pair is attached to the NTP (or the probe) for incorporation into the extension primer. Preferred binding partner pairs include, but are not limited to, biotin (or imino-biotin) and streptavidin, digoxinin and Abs, and Prolinx™ reagents.
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- In a preferred embodiment, chemical attachment methods are used. In this embodiment, chemical functional groups on each of the target sequences and adapter sequences are used. As is known in the art, this may be accomplished in a variety of ways. Preferred functional groups for attachment are amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly
25 preferred. Using these functional groups, the two sequences are joined together; for example, amino groups on each nucleic acid may be attached, for example using linkers as are known in the art; for example, homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference).
30 In a preferred embodiment, aptamers are used in the system. Aptamers are nucleic acids that can be made to bind to virtually any target analyte; see Bock et al., Nature 355:564 (1992); Femulok et al., Current Op. Chem. Biol. 2:230 (1998); and U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867, 5,705,337, and related patents, hereby incorporated by reference.
35 In a preferred embodiment, an array comprising capture probes that hybridize to adapter sequences is made, as outlined herein. In one embodiment aptamers, comprising adapter sequences, can be added. As will be appreciated by those in the art, the aptamers may be preassociated with their binding partners, e.g. target analytes, prior to introduction to the array, or not. In addition, the association between the adapter sequences on the aptamers and the capture probes can be made

covalent, for example through the use of reactive groups (e.g. psoralen) and appropriate activation.

In addition, the present invention is directed to the use of adapter sequences to assemble arrays comprising other target analytes.

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The adapter sequences may be chosen as outlined above. Preferably the adapters are selected from the sequences set forth in Table I, Table II, Table III or Table IV. These adapter sequences can then be added to the target analytes using a variety of techniques. In general, as described above, non-covalent attachment using binding partner pairs may be done, or covalent attachment using chemical 10 moieties (including linkers).

Advantages of using adapters include but are not limited to, for example, the ability to create universal arrays. That is, a single array is utilized with each capture probe designed to hybridize with a specific adapter. The adapters are joined to any number of target analytes, such as nucleic acids, as is 15 described herein. Thus, the same array is used for vastly different target analytes. Furthermore, hybridization of adapters with capture probes results in non-covalent attachment of the target nucleic acid to the address of the array (e.g. a microsphere in some embodiments). As such, the target nucleic/adapter hybrid is easily removed, and the microsphere/capture probe can be re-used. In addition, the construction of kits is greatly facilitated by the use of adapters. For example, arrays or 20 microspheres can be prepared that comprise the capture probe; the adapters can be packaged along with the microspheres for attachment to any target analyte of interest. Thus, one need only attach the adapter to the target analyte and disperse on the array for the construction of an array of target analytes.

25 Accordingly the present invention provides kits comprising adapters. Preferably the kits include at least 1 nucleic acid sequence as set forth in Table 1. More preferably the kits include at least 10-25 nucleic acids, with at least 50 nucleic acids more preferred. Even more preferable are kits that include at least 100 nucleic acids with more than 1000 even more preferred and more than 2000 even more preferred.

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It should also be noted that the sequences defined herein can also be used in "sandwich" assay formats, wherein a capture extender probe comprising a first domain that will hybridize to the capture probe and a second domain that has a target specific domain is used. The capture extender probe hybridizes both to the target sequence and the capture probe, thereby immobilizing the target 35 sequence on the array.

Once the adapter sequences are associated with the target analyte, including target nucleic acids, the compositions are added to an array comprising addresses comprising capture probes. In one embodiment a plurality of hybrid adapter sequence/target analytes are pooled prior to addition to an

array. All of the methods and compositions herein are drawn to compositions and methods for detecting the presence of target analytes, particularly nucleic acids, using adapter arrays.

Accordingly, the present invention provides array compositions comprising at least a first substrate with a surface comprising individual sites. The present system finds particular utility in array formats, i.e. wherein there is a matrix of capture probes (herein generally referred to "pads", "addresses" or "micro-locations"). By "array" or "biochip" herein is meant a plurality of nucleic acids in an array format; the size of the array will depend on the composition and end use of the array. Nucleic acids arrays are known in the art, and can be classified in a number of ways; both ordered arrays (e.g. the ability to resolve chemistries at discrete sites), and random arrays are included. Ordered arrays include, but are not limited to, those made using photolithography techniques (Affymetrix GeneChip™), spotting techniques (Synteni and others), printing techniques (Hewlett Packard and Rosetta), three dimensional "gel pad" arrays, etc. In one embodiment the ordered arrays include arrays that contain nucleic acids at known locations. That is, the adapters or capture probes described herein are immobilized at known locations on a substrate. By "known" locations is meant a site that is known or has been known.

In addition, adapters find use "liquid arrays". By "liquid arrays" is meant an array in solution for analysis, for example, by flow cytometry.

A preferred embodiment utilizes microspheres on a variety of substrates including fiber optic bundles, as are outlined in PCTs US98/21193, PCT US99/14387 and PCT US98/05025; WO98/50782; and U.S.S.N.s 09/287,573, 09/151,877, 09/256,943, 09/316,154, 60/119,323, 09/315,584; all of which are expressly incorporated by reference. While much of the discussion below is directed to the use of microsphere arrays on fiber optic bundles, any array format of nucleic acids on solid supports may be utilized.

Arrays containing from about 2 different bioactive agents (e.g. different beads, when beads are used) to many millions can be made, with very large arrays being possible. Generally, the array will comprise from two to as many as a billion or more, depending on the size of the beads and the substrate, as well as the end use of the array, thus very high density, high density, moderate density, low density and very low density arrays may be made. Preferred ranges for very high density arrays are from about 10,000,000 to about 2,000,000,000, with from about 100,000,000 to about 1,000,000,000 being preferred (all numbers being in square cm). High density arrays range about 100,000 to about 10,000,000, with from about 1,000,000 to about 5,000,000 being particularly preferred. Moderate density arrays range from about 10,000 to about 100,000 being particularly preferred, and from about 20,000 to about 50,000 being especially preferred. Low density arrays are generally less than 10,000, with from about 1,000 to about 5,000 being preferred. Very low density arrays are less than 1,000, with from about 10 to about 1000 being preferred, and from about 100 to about 500 being particularly preferred. In some embodiments, the compositions of the invention may

not be in array format; that is, for some embodiments, compositions comprising a single bioactive agent may be made as well. In addition, in some arrays, multiple substrates may be used, either of different or identical compositions. Thus for example, large arrays may comprise a plurality of smaller substrates.

5 In addition, one advantage of the present compositions is that particularly through the use of fiber optic technology, extremely high density arrays can be made. Thus for example, because beads of 200 µm or less (with beads of 200 nm possible) can be used, and very small fibers are known, it is possible to have as many as 40,000 or more (in some instances, 1 million) different elements (e.g. fibers and
10 beads) in a 1 mm² fiber optic bundle, with densities of greater than 25,000,000 individual beads and fibers (again, in some instances as many as 50-100 million) per 0.5 cm² obtainable (4 million per square cm for 5 µ center-to-center and 100 million per square cm for 1 µ center-to-center).

15 By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of beads and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates is very large. Possible substrates include, but are not limited to,
20 glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles; and a variety of other polymers. In general, the substrates allow optical detection and do not themselves appreciably fluoresce.

25 Generally the substrate is flat (planar), although as will be appreciated by those in the art, other configurations of substrates may be used as well; for example, three dimensional configurations can be used, for example by embedding the beads in a porous block of plastic that allows sample access to the beads and using a confocal microscope for detection. Similarly, the beads may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Preferred
30 substrates include optical fiber bundles as discussed below, and flat planar substrates such as glass, polystyrene and other plastics and acrylics.

In a preferred embodiment, the substrate is an optical fiber bundle or array, as is generally described in U.S.S.N.s 08/944,850 and 08/519,062, PCT US98/05025, and PCT US98/09163, all of which are expressly incorporated herein by reference. Preferred embodiments utilize preformed unitary fiber optic arrays. By "preformed unitary fiber optic array" herein is meant an array of discrete individual fiber optic strands that are co-axially disposed and joined along their lengths. The fiber strands are generally individually clad. However, one thing that distinguished a preformed unitary array from other fiber optic formats is that the fibers are not individually physically manipulatable; that is, one strand

generally cannot be physically separated at any point along its length from another fiber strand.

At least one surface of the substrate is modified to contain discrete, individual sites for later association of microspheres. These sites may comprise physically altered sites, i.e. physical

5 configurations such as wells or small depressions in the substrate that can retain the beads, such that a microsphere can rest in the well, or the use of other forces (magnetic or compressive), or chemically altered or active sites, such as chemically functionalized sites, electrostatically altered sites, hydrophobically/ hydrophilically functionalized sites, spots of adhesive, etc.

10 The sites may be a pattern, i.e. a regular design or configuration, or randomly distributed. A preferred embodiment utilizes a regular pattern of sites such that the sites may be addressed in the X-Y coordinate plane. "Pattern" in this sense includes a repeating unit cell, preferably one that allows a high density of beads on the substrate. However, it should be noted that these sites may not be discrete sites. That is, it is possible to use a uniform surface of adhesive or chemical functionalities, 15 for example, that allows the attachment of beads at any position. That is, the surface of the substrate is modified to allow attachment of the microspheres at individual sites, whether or not those sites are contiguous or non-contiguous with other sites. Thus, the surface of the substrate may be modified such that discrete sites are formed that can only have a single associated bead, or alternatively, the surface of the substrate is modified and beads may go down anywhere, but they end up at discrete 20 sites.

In a preferred embodiment, the surface of the substrate is modified to contain wells, i.e. depressions in the surface of the substrate. This may be done as is generally known in the art using a variety of techniques, including, but not limited to, photolithography, stamping techniques, molding techniques, 25 and microetching techniques. As will be appreciated by those in the art, the technique used will depend on the composition and shape of the substrate.

In a preferred embodiment, physical alterations are made in a surface of the substrate to produce the sites. In a preferred embodiment, the substrate is a fiber optic bundle and the surface of the substrate is a terminal end of the fiber bundle, as is generally described in 08/818,199 and 09/151,877, both of which are hereby expressly incorporated by reference. In this embodiment, wells are made in a terminal or distal end of a fiber optic bundle comprising individual fibers. In this embodiment, the cores of the individual fibers are etched, with respect to the cladding, such that small wells or depressions are formed at one end of the fibers. The required depth of the wells will depend on the size of the beads to be added to the wells. 35

Generally in this embodiment, the microspheres are non-covalently associated in the wells, although the wells may additionally be chemically functionalized as is generally described below, cross-linking agents may be used, or a physical barrier may be used, i.e. a film or membrane over the beads.

- In a preferred embodiment, the surface of the substrate is modified to contain chemically modified sites, that can be used to attach, either covalently or non-covalently, the microspheres of the invention to the discrete sites or locations on the substrate. "Chemically modified sites" in this context includes, but is not limited to, the addition of a pattern of chemical functional groups including amino groups, carboxy groups, oxo groups and thiol groups, that can be used to covalently attach microspheres, which generally also contain corresponding reactive functional groups; the addition of a pattern of adhesive that can be used to bind the microspheres (either by prior chemical functionalization for the addition of the adhesive or direct addition of the adhesive); the addition of a pattern of charged groups (similar to the chemical functionalities) for the electrostatic attachment of the microspheres, i.e. when the microspheres comprise charged groups opposite to the sites; the addition of a pattern of chemical functional groups that renders the sites differentially hydrophobic or hydrophilic, such that the addition of similarly hydrophobic or hydrophilic microspheres under suitable experimental conditions will result in association of the microspheres to the sites on the basis of hydroaffinity. For example, the use of hydrophobic sites with hydrophobic beads, in an aqueous system, drives the association of the beads preferentially onto the sites. As outlined above, "pattern" in this sense includes the use of a uniform treatment of the surface to allow attachment of the beads at discrete sites, as well as treatment of the surface resulting in discrete sites. As will be appreciated by those in the art, this may be accomplished in a variety of ways.
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- In a preferred embodiment, the compositions of the invention further comprise a population of microspheres. By "population" herein is meant a plurality of beads as outlined above for arrays. Within the population are separate subpopulations, which can be a single microsphere or multiple identical microspheres. That is, in some embodiments, as is more fully outlined below, the array may contain only a single bead for each capture probe; preferred embodiments utilize a plurality of beads of 10
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- each type.
- By "microspheres" or "beads" or "particles" or grammatical equivalents herein is meant small discrete particles. The composition of the beads will vary, depending on the class of capture probe and the method of synthesis. Suitable bead compositions include those used in peptide, nucleic acid and organic moiety synthesis, including, but not limited to, plastics, ceramics, glass, polystyrene, methylstyrene, acrylic polymers, paramagnetic materials, thoria sol, carbon graphite, titanium dioxide, latex or cross-linked dextrans such as Sepharose, cellulose, nylon, cross-linked micelles and Teflon may all be used. *"Microsphere Detection Guide"* from Bangs Laboratories, Fishers IN is a helpful guide.
- The beads need not be spherical; irregular particles may be used. In addition, the beads may be porous, thus increasing the surface area of the bead available for either capture probe attachment or tag attachment. The bead sizes range from nanometers, i.e. 100 nm, to millimeters, i.e. 1 mm, with beads from about 0.2 micron to about 200 microns being preferred, and from about 0.5 to about 5

micron being particularly preferred, although in some embodiments smaller beads may be used.

It should be noted that a key component of this embodiment of the invention is the use of a substrate/bead pairing that allows the association or attachment of the beads at discrete sites on the 5 surface of the substrate, such that the beads do not move during the course of the assay.

Each microsphere comprises a capture probe, although as will be appreciated by those in the art, there may be some microspheres which do not contain a capture probe, depending on the synthetic methods. Alternatively, some have more than one capture probe.

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Attachment of the nucleic acids may be done in a variety of ways, as will be appreciated by those in the art, including, but not limited to, chemical or affinity capture (for example, including the incorporation of derivatized nucleotides such as AminoLink or biotinylated nucleotides that can then be used to attach the nucleic acid to a surface, as well as affinity capture by hybridization), cross-linking, 15 and electrostatic attachment, etc. In a preferred embodiment, affinity capture is used to attach the nucleic acids to the beads. For example, nucleic acids can be derivatized, for example with one member of a binding pair, and the beads derivatized with the other member of a binding pair. Suitable binding pairs are as described herein for IBL/DBL pairs. For example, the nucleic acids may be biotinylated (for example using enzymatic incorporate of biotinylated nucleotides, for by 20 photoactivated cross-linking of biotin). Biotinylated nucleic acids can then be captured on streptavidin-coated beads, as is known in the art. Similarly, other hapten-receptor combinations can be used, such as digoxigenin and anti-digoxigenin antibodies. Alternatively, chemical groups can be added in the form of derivatized nucleotides, that can then be used to add the nucleic acid to the surface.

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Preferred attachments are covalent, although even relatively weak interactions (i.e. non-covalent) can be sufficient to attach a nucleic acid to a surface, if there are multiple sites of attachment per each nucleic acid. Thus, for example, electrostatic interactions can be used for attachment, for example by having beads carrying the opposite charge to the bioactive agent.

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Similarly, affinity capture utilizing hybridization can be used to attach nucleic acids to beads. For example, as is known in the art, polyA+RNA is routinely captured by hybridization to oligo-dT beads; this may include oligo-dT capture followed by a cross-linking step, such as psoralen crosslinking). If the nucleic acids of interest do not contain a polyA tract, one can be attached by polymerization with terminal transferase, or via ligation of an oligoA linker, as is known in the art.

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Alternatively, chemical crosslinking may be done, for example by photoactivated crosslinking of thymidine to reactive groups, as is known in the art.

In a preferred embodiment, each bead comprises a single type of capture probe, although a plurality of

individual capture probes are preferably attached to each bead. Similarly, preferred embodiments utilize more than one microsphere containing a unique capture probe; that is, there is redundancy built into the system by the use of subpopulations of microspheres, each microsphere in the subpopulation containing the same capture probe.

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In an alternative embodiment, each bead comprises a plurality of different capture probes.

As will be appreciated by those in the art, the capture probes may either be synthesized directly on the beads, or they may be made and then attached after synthesis. In a preferred embodiment, linkers 10 are used to attach the capture probes to the beads, to allow both good attachment, sufficient flexibility, to allow good interaction with the target molecule, and to avoid undesirable binding reactions.

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In a preferred embodiment, the capture probes are synthesized directly on the beads. As is known in the art, many classes of chemical compounds are currently synthesized on solid supports, such as 15 peptides, organic moieties, and nucleic acids. It is a relatively straightforward matter to adjust the current synthetic techniques to use beads.

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In a preferred embodiment, the capture probes are synthesized first, and then covalently attached to the beads. As will be appreciated by those in the art, this will be done depending on the composition 20 of the capture probes and the beads. The functionalization of solid support surfaces such as certain polymers with chemically reactive groups such as thiols, amines, carboxyls, etc. is generally known in the art. Accordingly, "blank" microspheres may be used that have surface chemistries that facilitate the attachment of the desired functionality by the user. Some examples of these surface chemistries for blank microspheres include, but are not limited to, amino groups including aliphatic and aromatic 25 amines, carboxylic acids, aldehydes, amides, chloromethyl groups, hydrazide, hydroxyl groups, sulfonates and sulfates.

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In a preferred embodiment the attachment of nucleic acids to substrates includes contacting the 30 oligonucleotide and the solid support in the presence of high salt concentrations. As is appreciated by those skilled in the art, salt includes, but is not limited to sodium chloride, potassium chloride, calcium chloride, magnesium chloride, lithium chloride, rubidium chloride, cesium chloride, barium chloride and the like. In a preferred embodiment, salt as used in the invention includes sodium chloride.

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By high salt concentrations is meant salt that is more concentrated than about 0.1 M salt. In a 35 preferred embodiment, by high salt concentrations is meant greater than about 0.2 M salt. In a particularly preferred embodiment, high salt concentrations include from about 0.5 to 3M salt, with about 1M to 2M being most preferred.

By solid support or other grammatical equivalents herein is meant any material that can be modified

to contain oligonucleotides. As will be appreciated by those in the art, the number of possible solid supports is very large. Possible solid supports include, but are not limited to beads, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.),
5 polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles, and a variety of other polymers.

Once formed, the support containing the oligonucleotides finds use in a variety of systems including
10 decoding arrays as described in more detail in U.S.S.N. 09/344,526, and U.S.S.N. 09/574, 117, both of which are expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in microfluidic systems as described in U.S.S.N. 09/306,369 which is expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in composite array systems as described in U.S.S.N. 09/606,369, which is expressly
15 incorporated herein by reference. In addition the support containing the oligonucleotides finds use in a variety of assays as outlined in more detail in U.S.S.N.s 09/513,362, 09/517,945, 09/535,854, 60/160,917, 60/180,810, 60/182,955, and 09/566,463, all of which are expressly incorporated herein by reference in their entirety. In addition, the support containing the oligonucleotides finds use in array based sensors as described in more detail in 09/287,573, 09/260,963, 09/450,829, 09/151,877,
20 09/187,289 and 08/519,062, all of which are expressly incorporated herein by reference in their entirety.

Accordingly the invention provides a method of attaching oligonucleotides to a solid support. The method includes contacting the oligonucleotides with the support in the presence of high salt as
25 described herein. Once attached, as discussed in the examples, the attached oligonucleotides readily hybridize to targets, probes and the like. Attachment of crude oligonucleotides in the presence of high salt is as efficient as attaching purified oligonucleotides. Thus, the invention also contemplates a method of attachment of oligonucleotides to a solid support without prior purification of the oligonucleotides. Again, the method includes contacting the crude oligonucleotides with a solid
30 support in the presence of high salt as described herein.

The capture probes are designed to be substantially complementary to the adapter sequences, to allow for a minimum of cross reactivity.

35 When microsphere arrays are used, an encoding/decoding system must be used. That is, since the beads are generally put onto the substrate randomly, there are several ways to correlate the functionality on the bead with its location, including the incorporation of unique optical signatures, generally fluorescent dyes, that could be used to identify the chemical functionality on any particular bead. This allows the synthesis of the candidate agents (i.e. compounds such as nucleic acids and

antibodies) to be divorced from their placement on an array, i.e. the candidate agents may be synthesized on the beads, and then the beads are randomly distributed on a patterned surface. Since the beads are first coded with an optical signature, this means that the array can later be "decoded", i.e. after the array is made, a correlation of the location of an individual site on the array with the bead or candidate agent at that particular site can be made. This means that the beads may be randomly distributed on the array, a fast and inexpensive process as compared to either the *in situ* synthesis or spotting techniques of the prior art.

However, the drawback to these methods is that for a large array, the system requires a large number of different optical signatures, which may be difficult or time-consuming to utilize. Accordingly, the present invention provides several improvements over these methods, generally directed to methods of coding and decoding the arrays. That is, as will be appreciated by those in the art, the placement of the capture probes is generally random, and thus a coding/decoding system is required to identify the probe at each location in the array. This may be done in a variety of ways, as is more fully outlined below, and generally includes: a) the use a decoding binding ligand (DBL), generally directly labeled, that binds to either the capture probe or to identifier binding ligands (IBLs) attached to the beads; b) positional decoding, for example by either targeting the placement of beads (for example by using photoactivatable or photocleavable moieties to allow the selective addition of beads to particular locations), or by using either sub-bundles or selective loading of the sites, as are more fully outlined below; c) selective decoding, wherein only those beads that bind to a target are decoded; or d) combinations of any of these. In some cases, as is more fully outlined below, this decoding may occur for all the beads, or only for those that bind a particular target sequence. Similarly, this may occur either prior to or after addition of a target sequence. In addition, as outlined herein, the target sequences detected may be either a primary target sequence (e.g. a patient sample), or a reaction product from one of the methods described herein (e.g. an extended SBE probe, a ligated probe, a cleaved signal probe, etc.).

Once the identity (i.e. the actual agent) and location of each microsphere in the array has been fixed, the array is exposed to samples containing the target sequences, although as outlined below, this can be done prior to or during the analysis as well. The target sequences can hybridize (either directly or indirectly) to the capture probes as is more fully outlined below, and results in a change in the optical signal of a particular bead.

In the present invention, "decoding" may not rely on the use of optical signatures, but rather on the use of decoding binding ligands that are added during a decoding step. The decoding binding ligands will bind either to a distinct identifier binding ligand partner that is placed on the beads, or to the capture probe itself. In this embodiment the decoding binding ligand either is complementary to the capture probe. In this embodiment the decoding binding ligand has the sequence of the adapter that also binds to the capture probe. In a preferred embodiment the decoder binding ligand is a nucleic acid

that has the sequence of at least one of the nucleic acids set forth in Table 1.

The decoding binding ligands are either directly or indirectly labeled, and thus decoding occurs by detecting the presence of the label. By using pools of decoding binding ligands in a sequential fashion, it is possible to greatly minimize the number of required decoding steps.

In some embodiments, the microspheres may additionally comprise identifier binding ligands for use in certain decoding systems. By "identifier binding ligands" or "IBLs" herein is meant a compound that will specifically bind a corresponding decoder binding ligand (DBL) to facilitate the elucidation of the identity of the capture probe attached to the bead. That is, the IBL and the corresponding DBL form a binding partner pair. By "specifically bind" herein is meant that the IBL binds its DBL with specificity sufficient to differentiate between the corresponding DBL and other DBLs (that is, DBLs for other IBLs), or other components or contaminants of the system. The binding should be sufficient to remain bound under the conditions of the decoding step, including wash steps to remove non-specific binding.

In some embodiments, for example when the IBLs and corresponding DBLs are proteins or nucleic acids, the dissociation constants of the IBL to its DBL will be less than about 10^{-4} - 10^{-8} M^{-1} , with less than about 10^{-5} to 10^{-8} M^{-1} being preferred and less than about 10^{-7} - 10^{-8} M^{-1} being particularly preferred.

IBL-DBL binding pairs are known or can be readily found using known techniques. For example, when the IBL is a protein, the DBLs include proteins (particularly including antibodies or fragments thereof (Fabs, etc.)) or small molecules, or vice versa (the IBL is an antibody and the DBL is a protein). Metal ion- metal ion ligands or chelators pairs are also useful. Antigen-antibody pairs, enzymes and substrates or inhibitors, other protein-protein interacting pairs, receptor-ligands, complementary nucleic acids, and carbohydrates and their binding partners are also suitable binding pairs. Nucleic acid - nucleic acid binding proteins pairs are also useful. Similarly, as is generally described in U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867, 5,705,337, and related patents, hereby incorporated by reference, nucleic acid "aptamers" can be developed for binding to virtually any target; such an aptamer-target pair can be used as the IBL-DBL pair. Similarly, there is a wide body of literature relating to the development of binding pairs based on combinatorial chemistry methods.

In a preferred embodiment, the IBL is a molecule whose color or luminescence properties change in the presence of a selectively-binding DBL. For example, the IBL may be a fluorescent pH indicator whose emission intensity changes with pH. Similarly, the IBL may be a fluorescent ion indicator, whose emission properties change with ion concentration.

Alternatively, the IBL is a molecule whose color or luminescence properties change in the presence of various solvents. For example, the IBL may be a fluorescent molecule such as an ethidium salt whose

fluorescence intensity increases in hydrophobic environments. Similarly, the IBL may be a derivative of fluorescein whose color changes between aqueous and nonpolar solvents.

In one embodiment, the DBL may be attached to a bead, i.e. a "decoder bead", that may carry a label such as a fluorophore.

In a preferred embodiment, the IBL-DBL pair comprise substantially complementary single-stranded nucleic acids. In this embodiment, the binding ligands can be referred to as "identifier probes" and "decoder probes". Generally, the identifier and decoder probes range from about 4 basepairs in length to about 1000, with from about 6 to about 100 being preferred, and from about 8 to about 40 being particularly preferred. What is important is that the probes are long enough to be specific, i.e. to distinguish between different IBL-DBL pairs, yet short enough to allow both a) dissociation, if necessary, under suitable experimental conditions, and b) efficient hybridization.

In a preferred embodiment, as is more fully outlined below, the IBLs do not bind to DBLs. Rather, the IBLs are used as identifier moieties ("IMs") that are identified directly, for example through the use of mass spectroscopy.

Alternatively, in a preferred embodiment, the IBL and the capture probe are the same moiety; thus, for example, as outlined herein, particularly when no optical signatures are used, the capture probe can serve as both the identifier and the agent. For example, in the case of nucleic acids, the bead-bound probe (which serves as the capture probe) can also bind decoder probes, to identify the sequence of the probe on the bead. Thus, in this embodiment, the DBLs bind to the capture probes.

In one embodiment, the microspheres may contain an optical signature. That is, as outlined in U.S.S.N.s 08/818,199 and 09/151,877, previous work had each subpopulation of microspheres comprising a unique optical signature or optical tag that is used to identify the unique capture probe of that subpopulation of microspheres; that is, decoding utilizes optical properties of the beads such that a bead comprising the unique optical signature may be distinguished from beads at other locations with different optical signatures. Thus the previous work assigned each capture probe a unique optical signature such that any microspheres comprising that capture probe are identifiable on the basis of the signature. These optical signatures comprised dyes, usually chromophores or fluorophores, that were entrapped or attached to the beads themselves. Diversity of optical signatures utilized different fluorochromes, different ratios of mixtures of fluorochromes, and different concentrations (intensities) of fluorochromes.

In a preferred embodiment, the present invention does not rely solely on the use of optical properties to decode the arrays. However, as will be appreciated by those in the art, it is possible in some embodiments to utilize optical signatures as an additional coding method, in conjunction with the

present system. Thus, for example, as is more fully outlined below, the size of the array may be effectively increased while using a single set of decoding moieties in several ways, one of which is the use of optical signatures on some beads. Thus, for example, using one "set" of decoding molecules, the use of two populations of beads, one with an optical signature and one without, allows the effective 5 doubling of the array size. The use of multiple optical signatures similarly increases the possible size of the array.

In a preferred embodiment, each subpopulation of beads comprises a plurality of different IBLs. By 10 using a plurality of different IBLs to encode each capture probe, the number of possible unique codes is substantially increased. That is, by using one unique IBL per capture probe, the size of the array will be the number of unique IBLs (assuming no "reuse" occurs, as outlined below). However, by using a plurality of different IBLs per bead, n, the size of the array can be increased to 2^n , when the presence or absence of each IBL is used as the indicator. For example, the assignment of 10 IBLs per bead 15 generates a 10 bit binary code, where each bit can be designated as "1" (IBL is present) or "0" (IBL is absent). A 10 bit binary code has 2^{10} possible variants. However, as is more fully discussed below, the size of the array may be further increased if another parameter is included such as concentration or intensity; thus for example, if two different concentrations of the IBL are used, then the array size increases as 3^n . Thus, in this embodiment, each individual capture probe in the array is assigned a 20 combination of IBLs, which can be added to the beads prior to the addition of the capture probe, after, or during the synthesis of the capture probe, i.e. simultaneous addition of IBLs and capture probe components.

Alternatively, the combination of different IBLs can be used to elucidate the sequence of the nucleic acid. Thus, for example, using two different IBLs (IBL1 and IBL2), the first position of a nucleic acid 25 can be elucidated: for example, adenine can be represented by the presence of both IBL1 and IBL2; thymidine can be represented by the presence of IBL1 but not IBL2, cytosine can be represented by the presence of IBL2 but not IBL1, and guanosine can be represented by the absence of both. The second position of the nucleic acid can be done in a similar manner using IBL3 and IBL4; thus, the presence of IBL1, IBL2, IBL3 and IBL4 gives a sequence of AA; IBL1, IBL2, and IBL3 shows the 30 sequence AT; IBL1, IBL3 and IBL4 gives the sequence TA, etc. The third position utilizes IBL5 and IBL6, etc. In this way, the use of 20 different identifiers can yield a unique code for every possible 10-mer.

In this way, a sort of "bar code" for each sequence can be constructed; the presence or absence of 35 each distinct IBL will allow the identification of each capture probe.

In addition, the use of different concentrations or densities of IBLs allows a "reuse" of sorts. If, for example, the bead comprising a first agent has a 1X concentration of IBL, and a second bead comprising a second agent has a 10X concentration of IBL, using saturating concentrations of the

corresponding labelled DBL allows the user to distinguish between the two beads.

Once the microspheres comprising the capture probes are generated, they are added to the substrate to form an array. It should be noted that while most of the methods described herein add the beads to the substrate prior to the assay, the order of making, using and decoding the array can vary. For example, the array can be made, decoded, and then the assay done. Alternatively, the array can be made, used in an assay, and then decoded; this may find particular use when only a few beads need be decoded. Alternatively, the beads can be added to the assay mixture, i.e. the sample containing the target sequences, prior to the addition of the beads to the substrate; after addition and assay, the array may be decoded. This is particularly preferred when the sample comprising the beads is agitated or mixed; this can increase the amount of target sequence bound to the beads per unit time, and thus (in the case of nucleic acid assays) increase the hybridization kinetics. This may find particular use in cases where the concentration of target sequence in the sample is low; generally, for low concentrations, long binding times must be used.

In general, the methods of making the arrays and of decoding the arrays is done to maximize the number of different candidate agents that can be uniquely encoded. The compositions of the invention may be made in a variety of ways. In general, the arrays are made by adding a solution or slurry comprising the beads to a surface containing the sites for attachment of the beads. This may be done in a variety of buffers, including aqueous and organic solvents, and mixtures. The solvent can evaporate, and excess beads are removed.

In a preferred embodiment, when non-covalent methods are used to associate the beads with the array, a novel method of loading the beads onto the array is used. This method comprises exposing the array to a solution of particles (including microspheres and cells) and then applying energy, e.g. agitating or vibrating the mixture. This results in an array comprising more tightly associated particles, as the agitation is done with sufficient energy to cause weakly-associated beads to fall off (or out, in the case of wells). These sites are then available to bind a different bead. In this way, beads that exhibit a high affinity for the sites are selected. Arrays made in this way have two main advantages as compared to a more static loading: first of all, a higher percentage of the sites can be filled easily, and secondly, the arrays thus loaded show a substantial decrease in bead loss during assays. Thus, in a preferred embodiment, these methods are used to generate arrays that have at least about 50% of the sites filled, with at least about 75% being preferred, and at least about 90% being particularly preferred. Similarly, arrays generated in this manner preferably lose less than about 20% of the beads during an assay, with less than about 10% being preferred and less than about 5% being particularly preferred.

In this embodiment, the substrate comprising the surface with the discrete sites is immersed into a solution comprising the particles (beads, cells, etc.). The surface may comprise wells, as is described

herein, or other types of sites on a patterned surface such that there is a differential affinity for the sites. This differential affinity results in a competitive process, such that particles that will associate more tightly are selected. Preferably, the entire surface to be "loaded" with beads is in fluid contact with the solution. This solution is generally a slurry ranging from about 10,000:1 beads:solution

5 (vol:vol) to 1:1. Generally, the solution can comprise any number of reagents, including aqueous buffers, organic solvents, salts, other reagent components, etc. In addition, the solution preferably comprises an excess of beads; that is, there are more beads than sites on the array. Preferred embodiments utilize two-fold to billion-fold excess of beads.

10 The immersion can mimic the assay conditions; for example, if the array is to be "dipped" from above into a microtiter plate comprising samples, this configuration can be repeated for the loading, thus minimizing the beads that are likely to fall out due to gravity.

15 Once the surface has been immersed, the substrate, the solution, or both are subjected to a competitive process, whereby the particles with lower affinity can be disassociated from the substrate and replaced by particles exhibiting a higher affinity to the site. This competitive process is done by the introduction of energy, in the form of heat, sonication, stirring or mixing, vibrating or agitating the solution or substrate, or both.

20 A preferred embodiment utilizes agitation or vibration. In general, the amount of manipulation of the substrate is minimized to prevent damage to the array; thus, preferred embodiments utilize the agitation of the solution rather than the array, although either will work. As will be appreciated by those in the art, this agitation can take on any number of forms, with a preferred embodiment utilizing microtiter plates comprising bead solutions being agitated using microtiter plate shakers.

25 The agitation proceeds for a period of time sufficient to load the array to a desired fill. Depending on the size and concentration of the beads and the size of the array, this time may range from about 1 second to days, with from about 1 minute to about 24 hours being preferred.

30 It should be noted that not all sites of an array may comprise a bead; that is, there may be some sites on the substrate surface which are empty. In addition, there may be some sites that contain more than one bead, although this is not preferred.

35 In some embodiments, for example when chemical attachment is done, it is possible to attach the beads in a non-random or ordered way. For example, using photoactivatable attachment linkers or photoactivatable adhesives or masks, selected sites on the array may be sequentially rendered suitable for attachment, such that defined populations of beads are laid down.

The arrays of the present invention are constructed such that information about the identity of the

capture probe is built into the array, such that the random deposition of the beads in the fiber wells can be "decoded" to allow identification of the capture probe at all positions. This may be done in a variety of ways, and either before, during or after the use of the array to detect target molecules.

- 5 Thus, after the array is made, it is "decoded" in order to identify the location of one or more of the capture probes, i.e. each subpopulation of beads, on the substrate surface.

In a preferred embodiment, pyrosequencing techniques are used to decode the array, as is generally described in "Nucleic Acid Sequencing using Microsphere Arrays", filed October 22, 1999 (no U.S.S.N. 10 received yet), hereby incorporated by reference.

In a preferred embodiment, a selective decoding system is used. In this case, only those microspheres exhibiting a change in the optical signal as a result of the binding of a target sequence are decoded. This is commonly done when the number of "hits", i.e. the number of sites to decode, is 15 generally low. That is, the array is first scanned under experimental conditions in the absence of the target sequences. The sample containing the target sequences is added, and only those locations exhibiting a change in the optical signal are decoded. For example, the beads at either the positive or negative signal locations may be either selectively tagged or released from the array (for example through the use of photocleavable linkers), and subsequently sorted or enriched in a fluorescence-activated cell sorter (FACS). That is, either all the negative beads are released, and then the positive 20 beads are either released or analyzed in situ, or alternatively all the positives are released and analyzed. Alternatively, the labels may comprise halogenated aromatic compounds, and detection of the label is done using for example gas chromatography, chemical tags, isotopic tags mass spectral tags.

25 As will be appreciated by those in the art, this may also be done in systems where the array is not decoded; i.e. there need not ever be a correlation of bead composition with location. In this embodiment, the beads are loaded on the array, and the assay is run. The "positives", i.e. those beads displaying a change in the optical signal as is more fully outlined below, are then "marked" to 30 distinguish or separate them from the "negative" beads. This can be done in several ways, preferably using fiber optic arrays. In a preferred embodiment, each bead contains a fluorescent dye. After the assay and the identification of the "positives" or "active beads", light is shown down either only the positive fibers or only the negative fibers, generally in the presence of a light-activated reagent (typically dissolved oxygen). In the former case, all the active beads are photobleached. Thus, upon 35 non-selective release of all the beads with subsequent sorting, for example using a fluorescence activated cell sorter (FACS) machine, the non-fluorescent active beads can be sorted from the fluorescent negative beads. Alternatively, when light is shown down the negative fibers, all the negatives are non-fluorescent and the positives are fluorescent, and sorting can proceed. The characterization of the attached capture probe may be done directly, for example using mass

spectroscopy.

Alternatively, the identification may occur through the use of identifier moieties ("IMs"), which are similar to IBLs but need not necessarily bind to DBLs. That is, rather than elucidate the structure of

5 the capture probe directly, the composition of the IMs may serve as the identifier. Thus, for example, a specific combination of IMs can serve to code the bead, and be used to identify the agent on the bead upon release from the bead followed by subsequent analysis, for example using a gas chromatograph or mass spectroscope.

10 Alternatively, rather than having each bead contain a fluorescent dye, each bead comprises a non-fluorescent precursor to a fluorescent dye. For example, using photocleavable protecting groups, such as certain ortho-nitrobenzyl groups, on a fluorescent molecule, photoactivation of the fluorochrome can be done. After the assay, light is shown down again either the "positive" or the "negative" fibers, to distinguish these populations. The illuminated precursors are then chemically 15 converted to a fluorescent dye. All the beads are then released from the array, with sorting, to form populations of fluorescent and non-fluorescent beads (either the positives and the negatives or vice versa).

20 In an alternate preferred embodiment, the sites of attachment of the beads (for example the wells) include a photopolymerizable reagent, or the photopolymerizable agent is added to the assembled array. After the test assay is run, light is shown down again either the "positive" or the "negative" fibers, to distinguish these populations. As a result of the irradiation, either all the positives or all the negatives are polymerized and trapped or bound to the sites, while the other population of beads can be released from the array.

25 In a preferred embodiment, the location of every capture probe is determined using decoder binding ligands (DBLs). As outlined above, DBLs are binding ligands that will either bind to identifier binding ligands, if present, or to the capture probes themselves, preferably when the capture probe is a nucleic acid or protein.

30 In a preferred embodiment, as outlined above, the DBL binds to the IBL.

In a preferred embodiment, the capture probes are single-stranded nucleic acids and the DBL is a substantially complementary single-stranded nucleic acid that binds (hybridizes) to the capture probe, 35 termed a decoder probe herein. A decoder probe that is substantially complementary to each candidate probe is made and used to decode the array. In this embodiment, the candidate probes and the decoder probes should be of sufficient length (and the decoding step run under suitable conditions) to allow specificity; i.e. each candidate probe binds to its corresponding decoder probe with sufficient specificity to allow the distinction of each candidate probe.

In a preferred embodiment, the DBLs are either directly or indirectly labeled. In a preferred embodiment, the DBL is directly labeled, that is, the DBL comprises a label. In an alternate embodiment, the DBL is indirectly labeled; that is, a labeling binding ligand (LBL) that will bind to the DBL is used. In this embodiment, the labeling binding ligand-DBL pair can be as described above for IBL-DBL pairs.

Accordingly, the identification of the location of the individual beads (or subpopulations of beads) is done using one or more decoding steps comprising a binding between the labeled DBL and either the IBL or the capture probe (i.e. a hybridization between the candidate probe and the decoder probe when the capture probe is a nucleic acid). After decoding, the DBLs can be removed and the array can be used; however, in some circumstances, for example when the DBL binds to an IBL and not to the capture probe, the removal of the DBL is not required (although it may be desirable in some circumstances). In addition, as outlined herein, decoding may be done either before the array is used to in an assay, during the assay, or after the assay.

In one embodiment, a single decoding step is done. In this embodiment, each DBL is labeled with a unique label, such that the number of unique tags is equal to or greater than the number of capture probes (although in some cases, "reuse" of the unique labels can be done, as described herein; similarly, minor variants of candidate probes can share the same decoder, if the variants are encoded in another dimension, i.e. in the bead size or label). For each capture probe or IBL, a DBL is made that will specifically bind to it and contains a unique tag, for example one or more fluorochromes. Thus, the identity of each DBL, both its composition (i.e. its sequence when it is a nucleic acid) and its label, is known. Then, by adding the DBLs to the array containing the capture probes under conditions which allow the formation of complexes (termed hybridization complexes when the components are nucleic acids) between the DBLs and either the capture probes or the IBLs, the location of each DBL can be elucidated. This allows the identification of the location of each capture probe; the random array has been decoded. The DBLs can then be removed, if necessary, and the target sample applied.

In a preferred embodiment, the number of unique labels is less than the number of unique capture probes, and thus a sequential series of decoding steps are used. In this embodiment, decoder probes are divided into n sets for decoding. The number of sets corresponds to the number of unique tags. Each decoder probe is labeled in n separate reactions with n distinct tags. All the decoder probes share the same n tags. The decoder probes are pooled so that each pool contains only one of the n tag versions of each decoder, and no two decoder probes have the same sequence of tags across all the pools. The number of pools required for this to be true is determined by the number of decoder probes and the n. Hybridization of each pool to the array generates a signal at every address. The sequential hybridization of each pool in turn will generate a unique, sequence-specific code for each candidate probe. This identifies the candidate probe at each address in the array. For example, if four

tags are used, then $4 \times n$ sequential hybridizations can ideally distinguish 4^n sequences, although in some cases more steps may be required. After the hybridization of each pool, the hybrids are denatured and the decoder probes removed, so that the probes are rendered single-stranded for the next hybridization (although it is also possible to hybridize limiting amounts of target so that the available probe is not saturated. Sequential hybridizations can be carried out and analyzed by subtracting pre-existing signal from the previous hybridization).

An example is illustrative. Assuming an array of 16 probe nucleic acids (numbers 1-16), and four unique tags (four different fluors, for example; labels A-D). Decoder probes 1-16 are made that correspond to the probes on the beads. The first step is to label decoder probes 1-4 with tag A, decoder probes 5-8 with tag B, decoder probes 9-12 with tag C, and decoder probes 13-16 with tag D. The probes are mixed and the pool is contacted with the array containing the beads with the attached candidate probes. The location of each tag (and thus each decoder and candidate probe pair) is then determined. The first set of decoder probes are then removed. A second set is added, but this time, decoder probes 1, 5, 9 and 13 are labeled with tag A, decoder probes 2, 6, 10 and 14 are labeled with tag B, decoder probes 3, 7, 11 and 15 are labeled with tag C, and decoder probes 4, 8, 12 and 16 are labeled with tag D. Thus, those beads that contained tag A in both decoding steps contain candidate probe 1; tag A in the first decoding step and tag B in the second decoding step contain candidate probe 2; tag A in the first decoding step and tag C in the second step contain candidate probe 3; etc. In one embodiment, the decoder probes are labeled *in situ*; that is, they need not be labeled prior to the decoding reaction. In this embodiment, the incoming decoder probe is shorter than the candidate probe, creating a 5' "overhang" on the decoding probe. The addition of labeled ddNTPs (each labeled with a unique tag) and a polymerase will allow the addition of the tags in a sequence specific manner, thus creating a sequence-specific pattern of signals. Similarly, other modifications can be done, including ligation, etc.

In addition, since the size of the array will be set by the number of unique decoding binding ligands, it is possible to "reuse" a set of unique DBLs to allow for a greater number of test sites. This may be done in several ways; for example, by using some subpopulations that comprise optical signatures. Similarly, the use of a positional coding scheme within an array; different sub-bundles may reuse the set of DBLs. Similarly, one embodiment utilizes bead size as a coding modality, thus allowing the reuse of the set of unique DBLs for each bead size. Alternatively, sequential partial loading of arrays with beads can also allow the reuse of DBLs. Furthermore, "code sharing" can occur as well.

In a preferred embodiment, the DBLs may be reused by having some subpopulations of beads comprise optical signatures. In a preferred embodiment, the optical signature is generally a mixture of reporter dyes, preferably fluorescent. By varying both the composition of the mixture (i.e. the ratio of one dye to another) and the concentration of the dye (leading to differences in signal intensity), matrices of unique optical signatures may be generated. This may be done by covalently attaching the

dyes to the surface of the beads, or alternatively, by entrapping the dye within the bead.

In a preferred embodiment, the encoding can be accomplished in a ratio of at least two dyes, although more encoding dimensions may be added in the size of the beads, for example. In addition, the labels
5 are distinguishable from one another; thus two different labels may comprise different molecules (i.e. two different fluors) or, alternatively, one label at two different concentrations or intensity.

In a preferred embodiment, the dyes are covalently attached to the surface of the beads. This may be done as is generally outlined for the attachment of the capture probes, using functional groups on the
10 surface of the beads. As will be appreciated by those in the art, these attachments are done to minimize the effect on the dye.

In a preferred embodiment, the dyes are non-covalently associated with the beads, generally by entrapping the dyes in the pores of the beads.

15 Additionally, encoding in the ratios of the two or more dyes, rather than single dye concentrations, is preferred since it provides insensitivity to the intensity of light used to interrogate the reporter dye's signature and detector sensitivity.

20 In a preferred embodiment, a spatial or positional coding system is done. In this embodiment, there are sub-bundles or subarrays (i.e. portions of the total array) that are utilized. By analogy with the telephone system, each subarray is an "area code", that can have the same tags (i.e. telephone numbers) of other subarrays, that are separated by virtue of the location of the subarray. Thus, for example, the same unique tags can be reused from bundle to bundle. Thus, the use of 50 unique tags
25 in combination with 100 different subarrays can form an array of 5000 different capture probes. In this embodiment, it becomes important to be able to identify one bundle from another; in general, this is done either manually or through the use of marker beads, i.e. beads containing unique tags for each subarray.

30 In alternative embodiments, additional encoding parameters can be added, such as microsphere size. For example; the use of different size beads may also allow the reuse of sets of DBLs; that is, it is possible to use microspheres of different sizes to expand the encoding dimensions of the microspheres. Optical fiber arrays can be fabricated containing pixels with different fiber diameters or cross-sections; alternatively, two or more fiber optic bundles, each with different cross-sections of the
35 individual fibers, can be added together to form a larger bundle; or, fiber optic bundles with fiber of the same size cross-sections can be used, but just with different sized beads. With different diameters, the largest wells can be filled with the largest microspheres and then moving onto progressively smaller microspheres in the smaller wells until all size wells are then filled. In this manner, the same dye ratio could be used to encode microspheres of different sizes thereby expanding the number of

different oligonucleotide sequences or chemical functionalities present in the array. Although outlined for fiber optic substrates, this as well as the other methods outlined herein can be used with other substrates and with other attachment modalities as well.

5 In a preferred embodiment, the coding and decoding is accomplished by sequential loading of the microspheres into the array. As outlined above for spatial coding, in this embodiment, the optical signatures can be "reused". In this embodiment, the library of microspheres each comprising a different capture probe (or the subpopulations each comprise a different capture probe), is divided into a plurality of sublibraries; for example, depending on the size of the desired array and the number of
10 unique tags, 10 sublibraries each comprising roughly 10% of the total library may be made, with each sublibrary comprising roughly the same unique tags. Then, the first sublibrary is added to the fiber optic bundle comprising the wells, and the location of each capture probe is determined, generally through the use of DBLs. The second sublibrary is then added, and the location of each capture probe is again determined. The signal in this case will comprise the signal from the "first" DBL and the
15 "second" DBL; by comparing the two matrices the location of each bead in each sublibrary can be determined. Similarly, adding the third, fourth, etc. sublibraries sequentially will allow the array to be filled.

In a preferred embodiment, codes can be "shared" in several ways. In a first embodiment, a single
20 code (i.e. IBL/DBL pair) can be assigned to two or more agents if the target sequences different sufficiently in their binding strengths. For example, two nucleic acid probes used in an mRNA quantitation assay can share the same code if the ranges of their hybridization signal intensities do not overlap. This can occur, for example, when one of the target sequences is always present at a much higher concentration than the other. Alternatively, the two target sequences might always be present
25 at a similar concentration, but differ in hybridization efficiency.

Alternatively, a single code can be assigned to multiple agents if the agents are functionally equivalent. For example, if a set of oligonucleotide probes are designed with the common purpose of detecting the presence of a particular gene, then the probes are functionally equivalent, even though they may
30 differ in sequence. Similarly, an array of this type could be used to detect homologs of known genes. In this embodiment, each gene is represented by a heterologous set of probes, hybridizing to different regions of the gene (and therefore differing in sequence). The set of probes share a common code. If a homolog is present, it might hybridize to some but not all of the probes. The level of homology might be indicated by the fraction of probes hybridizing, as well as the average hybridization intensity.
35 Similarly, multiple antibodies to the same protein could all share the same code.

In a preferred embodiment, decoding of self-assembled random arrays is done on the bases of pH titration. In this embodiment, in addition to capture probes, the beads comprise optical signatures, wherein the optical signatures are generated by the use of pH-responsive dyes (sometimes referred to

herein as "pH dyes") such as fluorophores. This embodiment is similar to that outlined in PCT US98/05025 and U.S.S.N. 09/151,877, both of which are expressly incorporated by reference, except that the dyes used in the present invention exhibits changes in fluorescence intensity (or other properties) when the solution pH is adjusted from below the pKa to above the pKa (or vice versa). In a preferred embodiment, a set of pH dyes are used, each with a different pKa, preferably separated by at least 0.5 pH units. Preferred embodiments utilize a pH dye set of pKa's of 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0, 10.5, 11, and 11.5. Each bead can contain any subset of the pH dyes, and in this way a unique code for the capture probe is generated. Thus, the decoding of an array is achieved by titrating the array from pH 1 to pH 13, and measuring the fluorescence signal from each bead as a function of solution pH.

Thus, the present invention provides array compositions comprising a substrate with a surface comprising discrete sites. A population of microspheres is distributed on the sites, and the population comprises at least a first and a second subpopulation. Each subpopulation comprises a capture probe, and, in addition, at least one optical dye with a given pKa. The pKas of the different optical dyes are different.

In a preferred embodiment, "random" decoding probes can be made. By sequential hybridizations or the use of multiple labels, as is outlined above, a unique hybridization pattern can be generated for each sensor element. This allows all the beads representing a given clone to be identified as belonging to the same group. In general, this is done by using random or partially degenerate decoding probes, that bind in a sequence-dependent but not highly sequence-specific manner. The process can be repeated a number of times, each time using a different labeling entity, to generate a different pattern of signals based on quasi-specific interactions. In this way, a unique optical signature is eventually built up for each sensor element. By applying pattern recognition or clustering algorithms to the optical signatures, the beads can be grouped into sets that share the same signature (i.e. carry the same probes).

In order to identify the actual sequence of the clone itself, additional procedures are required; for example, direct sequencing can be done, or an ordered array containing the clones, such as a spotted cDNA array, to generate a "key" that links a hybridization pattern to a specific clone.

Alternatively, clone arrays can be decoded using binary decoding with vector tags. For example, partially randomized oligos are cloned into a nucleic acid vector (e.g. plasmid, phage, etc.). Each oligonucleotide sequence consists of a subset of a limited set of sequences. For example, if the limited set comprises 10 sequences, each oligonucleotide may have some subset (or all of the 10) sequences. Thus each of the 10 sequences can be present or absent in the oligonucleotide. Therefore, there are 2^{10} or 1,024 possible combinations. The sequences may overlap, and minor variants can also be represented (e.g. A, C, T and G substitutions) to increase the number of possible

combinations. A nucleic acid library is cloned into a vector containing the random code sequences. Alternatively, other methods such as PCR can be used to add the tags. In this way it is possible to use a small number of oligo decoding probes to decode an array of clones.

- 5 As will be appreciated by those in the art, the systems of the invention may take on a large number of different configurations, as is generally depicted in the Figures. In general, there are three types of systems that can be used: (1) "non-sandwich" systems (also referred to herein as "direct" detection) in which the target sequence itself is labeled with detectable labels (again, either because the primers comprise labels or due to the incorporation of labels into the newly synthesized strand); (2) systems in
10 which label probes directly bind to the target analytes; and (3) systems in which label probes are indirectly bound to the target sequences, for example through the use of amplifier probes.

- Detection of the reactions of the invention, including the direct detection of products and indirect detection utilizing label probes (i.e. sandwich assays), is preferably done by detecting assay
15 complexes comprising detectable labels, which can be attached to the assay complex in a variety of ways.

- In a preferred embodiment, an array of different and usually artificial capture probes are made; that is, the capture probes do not have complementarity to known target sequences. The adapter sequences
20 can then be added to any target sequences, or soluble capture extender probes are made; this allows the manufacture of only one kind of array, with the user able to customize the array through the use of adapter sequences or capture extender probes. This then allows the generation of customized soluble probes, which as will be appreciated by those in the art is generally simpler and less costly.

- 25 When capture extender probes are used, in one embodiment, microsphere arrays containing a single type of capture probe are made; in this embodiment, the capture extender probes are added to the beads prior to loading on the array. The capture extender probes may be additionally fixed or crosslinked, as necessary.

- 30 Accordingly, the present invention provides compositions and methods for detecting the presence or absence of target analytes, including nucleic acid sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and soil samples); biological warfare agent samples; research samples (i.e. in the case of nucleic acids, the sample may be the products of an amplification reaction, including both target and signal amplification); purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.); As will be appreciated by those in the
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art, virtually any experimental manipulation may have been done on the sample.

The present invention provides compositions and methods for detecting the presence or absence of target nucleic acid sequences in a sample.

- 5 In a preferred embodiment, several levels of redundancy are built into the arrays of the invention. Building redundancy into an array gives several significant advantages, including the ability to make quantitative estimates of confidence about the data and significant increases in sensitivity. Thus, preferred embodiments utilize array redundancy. As will be appreciated by those in the art, there are
10 at least two types of redundancy that can be built into an array: the use of multiple identical sensor elements (termed herein "sensor redundancy"), and the use of multiple sensor elements directed to the same target analyte, but comprising different chemical functionalities (termed herein "target redundancy"). For example, for the detection of nucleic acids, sensor redundancy utilizes of a plurality of sensor elements such as beads comprising identical binding ligands such as probes. Target redundancy utilizes sensor elements with different probes to the same target: one probe may span the first 25 bases of the target, a second probe may span the second 25 bases of the target, etc. By building in either or both of these types of redundancy into an array, significant benefits are obtained.
15 For example, a variety of statistical mathematical analyses may be done.
- 20 In addition, while this is generally described herein for bead arrays, as will be appreciated by those in the art, this techniques can be used for any type of arrays designed to detect target analytes. Furthermore, while these techniques are generally described for nucleic acid systems, these techniques are useful in the detection of other binding ligand/target analyte systems as well.
- 25 In a preferred embodiment, sensor redundancy is used. In this embodiment, a plurality of sensor elements, e.g. beads, comprising identical bioactive agents are used. That is, each subpopulation comprises a plurality of beads comprising identical bioactive agents (e.g. binding ligands). By using a number of identical sensor elements for a given array, the optical signal from each sensor element can be combined and any number of statistical analyses run, as outlined below. This can be done for a
30 variety of reasons. For example, in time varying measurements, redundancy can significantly reduce the noise in the system. For non-time based measurements, redundancy can significantly increase the confidence of the data.
- 35 In a preferred embodiment, a plurality of identical sensor elements are used. As will be appreciated by those in the art, the number of identical sensor elements will vary with the application and use of the sensor array. In general, anywhere from 2 to thousands may be used, with from 2 to 100 being preferred, 2 to 50 being particularly preferred and from 5 to 20 being especially preferred. In general, preliminary results indicate that roughly 10 beads gives a sufficient advantage, although for some applications, more identical sensor elements can be used.

Once obtained, the optical response signals from a plurality of sensor beads within each bead subpopulation can be manipulated and analyzed in a wide variety of ways, including baseline adjustment, averaging, standard deviation analysis, distribution and cluster analysis, confidence interval analysis, mean testing, etc.

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In a preferred embodiment, the first manipulation of the optical response signals is an optional baseline adjustment. In a typical procedure, the standardized optical responses are adjusted to start at a value of 0.0 by subtracting the integer 1.0 from all data points. Doing this allows the baseline-loop data to remain at zero even when summed together and the random response signal noise is canceled out. When the sample is a fluid, the fluid pulse-loop temporal region, however, frequently exhibits a characteristic change in response, either positive, negative or neutral, prior to the sample pulse and often requires a baseline adjustment to overcome noise associated with drift in the first few data points due to charge buildup in the CCD camera. If no drift is present, typically the baseline from the first data point for each bead sensor is subtracted from all the response data for the same bead. If drift is observed, the average baseline from the first ten data points for each bead sensor is subtracted from the all the response data for the same bead. By applying this baseline adjustment, when multiple bead responses are added together they can be amplified while the baseline remains at zero. Since all beads respond at the same time to the sample (e.g. the sample pulse), they all see the pulse at the exact same time and there is no registering or adjusting needed for overlaying their responses. In addition, other types of baseline adjustment may be done, depending on the requirements and output of the system used.

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Once the baseline has been adjusted, a number of possible statistical analyses may be run to generate known statistical parameters. Analyses based on redundancy are known and generally described in texts such as Freund and Walpole, Mathematical Statistics, Prentice Hall, Inc. New Jersey, 1980, hereby incorporated by reference in its entirety.

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In a preferred embodiment, signal summing is done by simply adding the intensity values of all responses at each time point, generating a new temporal response comprised of the sum of all bead responses. These values can be baseline-adjusted or raw. As for all the analyses described herein, signal summing can be performed in real time or during post-data acquisition data reduction and analysis. In one embodiment, signal summing is performed with a commercial spreadsheet program (Excel, Microsoft, Redmond, WA) after optical response data is collected.

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Methods for signal summing and analyses are included in U.S.S.N. 08/944,850, filed October 6, 1997; 09/287,573, filed April 6, 1999; and 60/238,866, filed October 6, 2000; an PCT Nos. US98/21193, filed October 6, 1998; and US00/09183, filed April 6, 2000.

Once made, the methods and compositions of the invention find use in a number of applications. In a

preferred embodiment, the compositions are used to probe a sample solution for the presence or absence of a target sequence, including the quantification of the amount of target sequence present. The compositions and methods find utility in the detection of genotyping assays and sequencing assays, and in all sorts of target analyte assays, including immunoassays.

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For SNP analysis, the ratio of different labels at a particular location on the array indicates the homozygosity or heterozygosity of the target sample, assuming the same concentration of each readout probe is used. Thus, for example, assuming a first readout probe comprising a first base at the readout position with a first detectable label and a second readout probe comprising a second base at the readout position with a second detectable label, equal signals (roughly 1:1 (taking into account the different signal intensities of the different labels, different hybridization efficiencies, and other reasons)) of the first and second labels indicates a heterozygote. The absence of a signal from the first label (or a ratio of approximately 0:1) indicates a homozygote of the second detection base; the absence of a signal from the second label (or a ratio of approximately 1:0) indicates a homozygote for the first detection base. As is appreciated by those in the art, the actual ratios for any particular system are generally determined empirically.

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Generally, a sample containing a target analyte (whether for detection of the target analyte or screening for binding partners of the target analyte) is added to the array, under conditions suitable for binding of the target analyte to at least one of the capture probes, i.e. generally physiological conditions. The presence or absence of the target analyte is then detected. As will be appreciated by those in the art, this may be done in a variety of ways, generally through the use of a change in an optical signal. This change can occur via many different mechanisms. A few examples include the binding of a dye-tagged analyte to the bead, the production of a dye species on or near the beads, the destruction of an existing dye species, a change in the optical signature upon analyte interaction with dye on bead, or any other optical interrogatable event.

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In a preferred embodiment, the change in optical signal occurs as a result of the binding of a target analyte that is labeled, either directly or indirectly, with a detectable label, preferably an optical label such as a fluorochrome. Thus, for example, when a proteinaceous target analyte is used, it may be either directly labeled with a fluor, or indirectly, for example through the use of a labeled antibody. Similarly, nucleic acids are easily labeled with fluorochromes, for example during PCR amplification as is known in the art. Alternatively, upon binding of the target sequences, a hybridization indicator may be used as the label. Hybridization indicators preferentially associate with double stranded nucleic acid, usually reversibly. Hybridization Indicators include intercalators and minor and/or major groove binding moieties. In a preferred embodiment, intercalators may be used; since intercalation generally only occurs in the presence of double stranded nucleic acid, only in the presence of target hybridization will the label light up. Thus, upon binding of the target analyte to a capture probe, there is a new optical signal generated at that site, which then may be detected.

Alternatively, in some cases, as discussed above, the target analyte such as an enzyme generates a species that is either directly or indirectly optical detectable.

Furthermore, in some embodiments, a change in the optical signature may be the basis of the optical signal. For example, the interaction of some chemical target analytes with some fluorescent dyes on the beads may alter the optical signature, thus generating a different optical signal.

As will be appreciated by those in the art, in some embodiments, the presence or absence of the target analyte may be done using changes in other optical or non-optical signals, including, but not limited to, surface enhanced Raman spectroscopy, surface plasmon resonance, radioactivity, etc.

The assays may be run under a variety of experimental conditions, as will be appreciated by those in the art. A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding. Various blocking and washing steps may be utilized as is known in the art.

The following examples serve to more fully describe the manner of using the above-described invention, as well as to set forth the best modes contemplated for carrying out various aspects of the invention. It is understood that these examples in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references cited herein are incorporated by reference in their entirety.

Examples**Example 1****Immobilization of Crude Oligonucleotides to a Solid Support**

1. Introduce chemical functional group (such as -NH₂, -COOH, -NCO, -NHS, -SH, -CHO, etc.) onto
5 solid support.

2. Activate the functional group before oligonucleotide attachment.

3. 5'-terminal modified oligonucleotide attachment.

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Crude Oligonucleotides were attached to supports and compared to results from attachment of purified oligonucleotides. As demonstrated in Figure 3, in the presence of 2M salt, crude oligonucleotides were immobilized as efficiently as purified oligonucleotides.

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IN addition, the improved attachment of oligonucleotides to a solid support in the presence of increased salt was sequence and length independent. Thus, the method finds use in attachment of all oligonucleotides to a solid support (see Figure 4).

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In addition, when 0.5 M to 3 M NaCl was used for attachment of oligonucleotides, non-purified oligonucleotides were attached with comparable efficiency when compared to purified oligonucleotides (see Figure 5).

TABLE 1

Sq. No.	Sequence (5'→3')
17	GGCTGGTTCGGCCCCGAAAGCTTAG
18	GTTCCCAGTGAAGCTGCGATCTGG
19	TACTTGGCATGGAATCCCTTACGC
20	ACTAGCATATTCAGGGCACCGGC
21	GAACGGTCAATGAACCCGCTGTGA
22	GCGGCCCTGGTCAATATGAATCG
23	GATCGTTAGAGGGACCTTGCCCAGA
24	TGGACCTAGTCCGGCAGTGACGAA
25	ATAAACTACCCAGGACGGGCGGAA
26	CATCGTTCGCGCCAATCCAGATA
27	GTCGGGCATAGAGCCGACCACCC
28	CTTGGGTCATGATTACCGTGCTA
29	TGCCTAACGTGCTAATCAGCAGCG
30	CGCATGTTGGAGCATATGCCCTGA
31	AGCCACTGCATCAGTGTGTTCAA
32	GGTTGTTTGAGGGCTCCACACT
33	TCGACCAAGAGCAAGGGCGGACCA
34	GACATCGCTATTGCGCATGGATCA
35	GAAATACGAAGTCTGCGGGAGTCG
36	TGTCATGAATGATTGATCGCGCGA
37	ATATCGGGATTGCGTCCCGGTGAA
38	GCGAGCGTACCGAAGGGCCTAGAA
39	TTACCGGCAGCGGACTTCCGAATT
40	GTAATCGAGAGCTGCGCGCGTCT
41	TCCCTGAGGTGCGAAGCTTCCGAC
42	CCTGTTAGCGTAGGCGAGTCGATC
43	TAGCGGACCGGCAGAATGAGTTCC
44	GGTACATGCACTACGCGCACTCGG
45	AATTCACTCGGACTCCCGCGGTA
46	GCCAAATCTGGATTGGCAGGAATG
47	TGCATTTCGGTTGAGGCACATCC
48	CCGCTCAATTACCATGCTTCGCT
49	CTCGGAAAGGTGCAACTTGGTGT
50	AATTGCGACCAGCAGAACGTCCT
51	GCCAGAGTCTCAACCTCACGGGAT
52	CCAACAACTGGAACGGGAACCCGC
53	GAGAACTGATCGCTGAGGGGCATG
54	GGCACACTAGACTTGTGGCACCGA

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55	CTTGGGCAAACGCTTCAGCCACAA
56	TCACATCCAAATATGGTCCCGCAA
57	GTCTGCCGGTGTGACCGCTTCATT
58	CATCGCAGAGCATAAACACCCCTCA
59	GTTGGTATCTATGGCAGAGGCGGA
60	ACGAGGTGCCGCTGAGGTTCCATT
61	GGAATGAGTGGACCCAGGCACATT
62	TGTCAATATGCGTCCGTGTCGTCT
63	TGATGAGCCTCAGGGTACGAGGCA
64	CACCCGGTGTTCCTACAGAATGA
65	TTGTTGCCAATGGTGTCCGCTCGG
66	TTAACCTGCGTCTGCCCCCTTCCT
67	AGGCCGTTCCCTGCCTTAGTGACG
68	TAGGGCGATGGCACGAAGCTCAA
69	TGCATAGAGCCAAAGTCGGCGATG
70	TTGAGAGGCAGGTGGCCACACGGA
71	TCCGCATTGTGAGAAAAAACGAGC
72	GGCGGTTCCGTAGCTATAGGTGC
73	GGTAAAATTTCGTAGCCACGGGC
74	CCGACGGAGGATGAAGACAATCAC
75	CCAGTTGGCCCAATTGCCAAAAA
76	GGATCTATTAGGCCGTGCCACAG
77	CGGATGTCACCGTTGGACTTCA
78	ATCGCAAATCCTGCTCGTCCCTAA
79	CAGGGCATGCAATAATCGAGGTTTC
80	CATGCGTTGATATATGGGCCAAG
81	CAGCTGCAGCTTGTGACCAACCAC
82	TTGTATGTCTGCCGACCGGCGACC
83	GATGGCGCCC GTT GATAGGTATGG
84	ATGAGAATGCCGGCAATCTGCTA
85	ATTTGCACTGACCGCAGGCTCGTG
86	CAGGGAGAACGGTTAAGTCCCCT
87	AGGCCGGCGATCGAGGAGTTGGT
88	ACACGGTGGTCTCTGATAGCGACC
89	GTGCAACGCCGAGGA CTTCCATCA
90	TCGGTGCCTGATAGCCATTCCGAT
91	TGAAATACCAACACAGCCAATTGGC
92	GCATCGTGTACATGACTGCCGCGA
93	CAGTGTCTAACGGCGCGTGAA
94	CGCTTGCAACGTTGCACCTACTCT
95	CGAAAAACTAGTGGCTCGCCGCG
96	CTTTCAGGGAACTGCCGGAGTCG

	97	TTGTGCCCTTCTTGTAAAGGCACG
5	98	TCCACGAACGGCGACCGTTGTCT
	99	CGACCTTGCACGAAACCTAACGAG
	100	GTGCAGCTTCACGAGCCAGCCTGA
	101	CGCTTCGTGCGAATAGACGATGA
	102	TGCGCTTACAGGCTCCTAGTGGTC
	103	CACGCGCTTAGTCGCGATCGCATA
	104	CGGAGGGAGGGAGCTAGCCTTCGA
10	105	GCATCCGGCCTGTTGATGACGCCT
	106	AGGCCAATCGATCTTATTGCCGAG
	107	CCTTCCAATGATTGCATA CGCCCCA
	108	AACACTTGATCAGGCGGGTCGTCT
	109	TGGAATCAAGGCCGTAAAGGACAG
15	110	GCTCCCGTAACCTGTCCACCAGTG
	111	AGTGGTGAATGCCGCTACCGCTGA
	112	TGTTGAAGCGAGCTAAAACGGCCA
	113	CAGCGCTCCAGAATTGACAGCAAT
	114	AAGGTGGTGCCATTCA TTGGCTA
	115	CGTTAAACCGCAATCCGTTGGCT
20	116	TGTCTCCACCTCGAAGGTTCCA
	117	CACGAGATA CCGCGTAAGGGTGG
	118	CTACGGCAAACGTGTGGAATGGGT
	119	GTAGGGCGATGACGGCGAACTAC
	120	AATCGACCTCCGCACACATTGCA
25	121	GAGTCAGCATGGCGGCGGAGATT
	122	AGATAAAGACGCTGGCAACACGGG
	123	GGTACCTCAACCGCAACCAC TTGT
	124	AAGCGATGGCTACCCAAGAGCGAT
	125	AGAGCTTATGCAGAACCCAGGGGCC
30	126	ATCGGTCTCACGCAGGGTTGGATA
	127	TAGGTTGCCGCCAGAAGAAACAT
	128	CGGTGCTGTTGCAAAGCCTGTAG
	129	TGATGAAAGTTGCGGCAGGACAC
	130	GTTGAGTGCAGGATGCAGCGATAG
35	131	AACATTGCGCGGTCCACCAAGGGTT
	132	GGGCAGTTAGAGAGGGCCAGAAGT
	133	TCGAGCTGGTCCCCTGAACGTGT
	134	GTCTGGGGGCCGCTAGTGAAAA
	135	ACTGTTGGCTTGCCTCATGTCCA
40	136	AGGACCATTCGGAAGGCGAAGATA
	137	CTTGGGAGGCATCCGCTATAAGGA
	138	AATAAACGGAACGCACCGCTACAG

	139	TTGTACGTGCGGTCCCCATAAGCA
5	140	CGCACCAAATGAGTTCCAGAC
	141	ACCTGATCGTCCCCTATTGGAA
	142	GGAACAGAGGCCAGGGGACTGAGC
	143	CCCTGCCTTGGCGTGTGGCTTAT
10	144	ACTCTGACACGCCAACCTCCGGAAG
	145	CTGACGGTTTCATTGGCGTGCC
	146	TGCGGTGGTCATTGGAGCTGGCC
	147	GCATGGCCAATCTAGTGACTCGCAA
15	148	AGGCCGTAAAGCGAATCTCACCTG
	149	CGAATATTATGCCGAGAACCGCG
	150	ACAGACGAGCTCCAACCACATGA
	151	GGACGGTTGTGCTGGATTGTCTG
	152	AAAGGCTATTGAGTTGGTGGCG
20	153	GATGGCCTATTGGAGATCGGCC
	154	GATCCAGTAGGCAGCTTCATCCA
	155	AATAACTCGCGCGGTATGCTTCT
	156	GGAGGAGGTTGTCTGGAAAGCA
	157	CTTGTTGATGGCACATGCTGCCG
25	158	AGAAAGGCTCGAGCAACGGGAAC
	159	AATCTACCGCACTGGTCCGCAAGT
	160	CGTGGCGGCCACAGTTTGGAGG
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	676	CTCATCGCTTAACACGAGAGCCC
35	677	AATGGCACTTCGGCGGTGATGCAA
	678	CCGTGGGAGGGAAATCCAACCGAGG
	679	AAATTCTCGTTGGTACGGCTCAT
	680	TTGCTCTTATCCTTGTCTGGCG
	681	TTAAGGATCAGGCGGAGCTTGCAG
40	682	CGCGACTAAGGTGCTGCAACTCGA
	683	GCTCGATTTCACGGCCGTTGTT
	684	AGCAGAGTGCCTGCAGAGGCTAA

5	685	TGGAGGTGAGGACGACGTGCACTA
0	686	AACCGTTAGGGTACATTGGCGGT
5	687	TATGATCGCTCGGCTCACAGTTG
20	688	GACTTTGCGGAAACGTCATGGT
25	689	TGTCGGTTATTCCACCTGCAAGGA
30	690	CTATGGTTGCACTGCGCCGTCGA
35	691	AGCAGGGAAATTCAATCGTTCGCA
40	692	CCTAACCGAGCGCTTAGCATTCC
685	693	CCCGACCCCTAACTCGCATTGAATA
686	694	TTGCTTAATGGTGACGCCACGGAT
687	695	GATGCTCGCCGTGTTAGTTACCG
688	696	TCGGATGACGAGTTCCATGACGG
689	697	ATGCGGTCTACTTCTGATCGGG
690	698	TTGCGAGGCTAACGACACGGTAAA
691	699	AACTTAATTACCGCCTCTGGCGCC
692	700	GTGACCGCGAACTTGTCCGACAG
693	701	TGCGGATTACCGATTGCGCTTTAA
694	702	TGATAGGGGCCACGTTGATCAGA
695	703	TCGCTCCGTAGCGATTCATCGTAG
696	704	TGTCAGCTGGTAGCCTCCGTTGA
697	705	AGCGTCGCATGACGCTTACGGCAC
698	706	TCACTCAGCGCTGTGACTGCCTGA
699	707	GTTTGCCTATAGTGGGGGACCGT
700	708	GTCGCATTCTGCACTGGCTCGCC
701	709	TGATTAGGTGCGGTCCCGTAGTCC
702	710	AAGGGACCTTGGGTGACGGCGAGA
703	711	TCAAATGGCCACCGCGTGTCAATT
704	712	CTCCGACGACCAATAATAGCCGC
705	713	GGCTATTCCCGTAGAGAGCGTCCA
706	714	TGGATAACCTCTGGTCCATCCAC
707	715	GACCGCTGTACGGAGTGTGCCTT
708	716	GCCACAGAGTTTAGCAGGGACCC
709	717	CCCACGCTTCCGACCACTGACCT
710	718	CATTGACACAAATGCGGGGACTGAT
711	719	AGCCACTCGACAGGGTCCAAAGC
712	720	CAGGATGAGCAAAGCGACTCTCCA
713	721	CAAGGTATGGTCTGGGGCCTAAGC
714	722	GGTGTGCGCCTAAACTCTTCGG
715	723	TTTAGTCGGACCCGTGGCAATT
716	724	CACACGTTCCGACCAGCCTGAAC
717	725	CTGGACGAACTGGCTCCTCGTAC
718	726	TTCACAATCCGCCGAAAATGACC

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727	AACAGGATATCCCGCGATCACGACA
728	TACGTCGGATCCATTGCGCCGAGT
729	CATGGATCTCTCGGTTTGTGCC
730	AGCCAGGCGCGTATATACTCGG
731	ATTTGGCACGTGTCGTGCCATGTT
732	CCCGCGTTGCACCACCTTGAGGTGC
733	TTGGACGTGACAAGCATGGCGCTC
734	CTGAATCGCGCAAGTAAATGGGGG
735	GATAAGGTCCACCAAGATTGCGCGC
736	CTAACAAATTGCCAACCGGGACGGC
737	GGTAACCTGGGTGCTTGCAAGGTTA
738	ATCGGAGCCACCATTGCGATTGGG
739	GTGAACCTGGCTTCCCCAGGATT
740	AGGCGATAGCATGGTCCCATATGA
741	AACGGTATCGTGGCTAATGCACGA
742	AGTAGTGGTCCTCCAGATGGCAA
743	CCGTTGAATTGGACGGGAGGTTAG
744	GCATAAGTGCAGGCATCGCGAAGGG
745	CGACAAGATGCAGCTGCTACATGC
746	TCGCAGTGATTCCCGACCGATAAG
747	CAAGGGAGTCCACTCGAGGGGAC
748	GCAACTTGACGGCATAAGTGGCC
749	TCCGAGCTTGACGTTGCGACGTC
750	AGCGCTGGCTGTGCTGCCATCTC
751	TTCATGTCGCTGAGTAACCCCTCGC
752	CGAACCGCTAATGCCATTGTCAG
753	CACGGAAGGTGGACAAATGCCG
754	CACAGATGGAGACAAACGCCCTT
755	TTTCGCAACTCGCTCCATAACCC
756	ACGTTACGTTCCGGCGCTCTAA
757	TATCGGATTGCGTGGGTTCAATC
758	CTTCCACAATTGTCGACGAC
759	TGCACAAAGGTATGGCTGCCGGC
760	ACCGTGGCCGGGCCATAAGCTACG
761	TCCGATGCCAGTCCCATCTTAAGA
762	CTGAAACCGTGCAGTCAAGGTGA
763	CGGTGTTCCCGCGTGTGAAAAAAT
764	TCTAGCAGGCCTTGAATCGCCA
765	GAGTCACCTCTGAGACGGACGCCA
766	TCTTCTGTCATCCTGCAGCAGCAT
767	GCGGATGAAACCTGAAAGGGCCT
768	GGGGCCCCAAACTGGTATCAAGCC

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769	GCATTGGCTTCGGATTCTCCCTACA
770	AGGCGGCCAACGTGAGGTCTTG
771	ACACCATGTGCTCCGCGCTGCAGT
772	ACGATGAACATGAATCGGGAGTCG
773	CTGCATCCCTGTAGCAGCGCTCCG
774	GTGCCGTATTCGACCTGTGCGTT
775	GCAGTGCAGCACTTCAGTTCAAAG
776	GCGATTTAACGCGATGCCTTGACG
777	TAGGTGACCTAGGCTTGCTTGGG
778	CTGGATACCTGCTGTGCGGCGC
779	CCCCTTACGGCTCGTCGTCTATGC
780	GCGCTTGGCCGATGCATGCATTA
781	TTTCTGTAAGCGGGCTGGGTTCA
782	GGCTGAGGTGAGCGGTAAGGATGA
783	TCTTGGCCTCCCCGATCTAATTG
784	GGAGGTAACGCCGTGTACGTAGGA
785	GTAATCCATTGTGGCTGCGTCAA
786	CAAACCCATTCCAGCAGACGCCTG
787	TAGGAGGAATTGGCATGCGGGCG
788	ATAGGTAGGATGTGCCGGCGTTG
789	GCAAGTGCTTAGCTCGTCAGCCTC
790	CTGGCTGTGCGCATCTCGTTAAC
791	CTAACGTCGTCTCGCGCAATCACT
792	TTTCATAAACGTTGTCCCCGAGC
793	AGCAGGAGGACGAACCTCCGCTCC
794	TTCAAGCACCATCGTGCAATCCAA
795	AGCGTCGCCAGTGATCGCTAGTGG
796	TACATTCCCTGCCCTCGTGGCCTT
797	CGCTTCGCGTATTCACTAGCGGTT
798	TCGGACGCGTCGACACTCATTATA
799	TCTGAGCAGGCCAGCGCTCCAGCT
800	TTGAATTGCCAAGCCCTGAAAGCC
801	AGTTTTCGCCCTGATGCGTCGGTG
802	GTTTCATAGGCCACGCGTGTAAA
803	GGAGCGAAGACTTCGTCTGCCAA
804	ATTGGCCGAGGGTGAATGCAGCCT
805	TGATCCATCCGAATGCTTTCCAT
806	GCACACAGTTGCTTGGCCCATGA
807	CTGGCGGGCAGTGGAAAAAACAAC
808	ATCTCCATGCGTAAGACTGCTCCG
809	TCTCCTCTCGTCGAGTTCGTGGA
810	TAGCGTATTCACTCTGCCGAGCA

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811	CAATCAAAGCCACGGCGCGATGG
812	AGCGTCACGGAATTCAAGCAGATCT
813	GACTCCCTGTTAATGCGCCAAGG
814	TAGGCACTGCCGGTTCAGATTCAA
815	AACAGGGTGATAACGGTGGCCAAT
816	CGTGCCTACCATGTGTAAGTGCCTG
817	GACCAATTCTACTTCGGCAGCCCCA
818	ATCGGACCGATTGCTTTGGCTG
819	TCCGCCGAAGCACACGCTTATTCTG
820	AACGGTACGCATTGTGAGCAGTGT
821	TGGCGACTACTGTTCCCTGAATC
822	CAGAGGGGACAGCCGTATGCCCTA
823	CGGTGGTTTATCGGAATCTGCGA
824	TTGGCCTCCGACCTCACGACATAT
825	CGTTTCGCTAGCATCTGGCGCCGA
826	ACTAACGGTGGAGCCGGTGGATG
827	ATATTGGCTGCCTTACGGGCCGC
828	CCGCTATGGTGGCAATCCCATAAC
829	GTTGCATGTGGCTCAGGCGGCATA
830	ATTCTGGGAGTGACCCAGGGCTT
831	CTCTCCAAGGAGAGCAGCCAATGT
832	GAAAGGACGGGATTGGGGCTAA
833	TATGTAGTACCTGGCTCGCGCCA
834	TCCCTTCGATGAGCGGCTGTACT
835	TAGATCGGGCAGAGCCCCTATCTT
836	GGAATGCTTAGGCTGCCGAGCTG
837	ATGGTAGCAACATTCAACGCCAGG
838	CTATGAAACGTGGCCCAAGCAAC
839	ATGTTGCTAGTGCCTTCGGGCCT
840	CCAATGTGCGCAGACTCAGTCATT
841	GATAGTGCCTCGCAAACGGGCCTTC
842	GCACCCCTGTTGCCTCATTGAGCGT
843	GGCGTGAATAGAGTGACCAGGCGG
844	ACGTGCCAGCTGCCGGACTTTAT
845	AGTGGAAATAGTCGCGTCGTGCCGC
846	ACTCGCCTATTACCGCTGGATTGG
847	GAGACCGGATTGAGATGATCCCCT
848	AAAATGGCAGGCCGGCAAGCAATTG
849	CTGGCAGTTACCAACCGAACAGT
850	TTACATTGCCGATTTCGCTGTGA
851	TAAAACGTGAAGGGTGCCTCAGCA
852	GGCTTCGCATGCCCTTGCAACATT

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853	AAGACCGAAGGTCTCTCTGAGGGC
854	GCCTATGGCTCCAGCTCAGCAGTA
855	CGTATCATAGCGTCGGTGGACAA
856	CATGCGCTCGCACTCTGCCTGTCT
857	TGGGCAATTGGAAACGTCGGTCT
858	TTGCGGAGATGCGACGGTACATTG
859	ACTTCGCACGTCGATCTGGACTG
860	CTAACTGCCGCGGAAACTGATTA
861	GGCCGCGGATTTATTCCCTGGAT
862	GAATTGGAACGGTGTCCGATGA
863	GTCCATCCATCTACGGCATCAGGA
864	TAAACGACCTGGCACATGTGCGTA
865	CACCATCCAAGAGCCAATCCTAGG
866	ACTCATATACGATCAGTCCGCCGC
867	GTGCCAACCGACGATCAACCGAAC
868	TGGGGTTCGTACAGGTGGTTCAT
869	AACAGTAGAGGCAGGGCTGCGGG
870	TGCATCGAATCCGAGATGGATCTT
871	GCGTCACGTTATGTCCGCTCTGTC
872	GGGACATGCGTAGCGCAATATCAC
873	CACACGTACACCATCCAAAGTGG
874	ATGCTCAGGTGCTAAATACGGCCA
875	AAAAATGTTAGCCGCGTACTGG
876	ATAGTCCGTTCCGTTCCAACGA
877	TCGATCTCTGGGTTGCAGACCAG
878	GTCGGCGCAGCCGATCCTCATGTC
879	GTTGCGGGGTGTGCAAAGGATCT
880	ATCTCTCCTCGGGTGGATGCCAG
881	TGATGTGCGTTAGCTTCGCG
882	GTAAAGGGGTGAGAACATCCGGCC
883	AAGTCGTCTCCCTGCGTCTCGTCC
884	CCGACCTAATAAGGCGCAACAATG
885	CATCATTGGCACCGTACCAATGCC
886	TGGAGAAAGGGAAAGTGCAGCAACG
887	TGGTACTCCTGTCATGCCTGCCA
888	GGCACAGGTTCTTGCGAGCGCGG
889	GAATCTGGGCATTGCTACGAGACC
890	CGAAATGGGAGCGTCCACTACCAC
891	ACATATGAGCTCGCGTGCTTGCAT
892	TCGAGCACGGTCACTGATAAAGCC
893	GAGGGTCCCTGCTCAGAGTTGGTT
894	AAATGCGATCGCCCCCTATGGAAT

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895	CTACCCGAATGGATTGCGGATGGC
896	AGGGACTGGCAGGTCTCTGCGCGT
897	TAACGATCCATTCCACGAATGCAG
898	GGCCGCACGTACGATTACGCCCTG
899	TGGGAAATGCATCAGTTGTTGGCT
900	TATCTGGGAGTAGCAGGCAGGGCC
901	CCGAAGGTTTCACGCTCAGGT CGC
902	GAACCCAGCTGGGACATCCTTCAG
903	TGCATGCGAGCAAATAACCCGGAC
904	AATTGTCCGCCAAACGCTTTCA G
905	GTCGGCTTCGAGCGATCGAGTG TG
906	TCGCGTGCTCTACGTAGCCC ATGA
907	GGCTTCCCGCGATAACGTAATT CGC
908	TGTAGCCGACTAGGGCCGAAGCCC
909	AAGCGAACGCCCTGGCTGAATATT
910	TGTCACCGCAGCTGCTGCAGATT T
911	CCGTGTCCGTGTTGTCGACAGGC G
912	CCCCACACGTTGCGCCTATATGTG
913	GGCGGGCACAACTCAACACAGATG
914	CGACTGCGGGATCACCGGTGATTA
915	TCGGGACATGACCGGTACGGAGTC
916	TACCTCGAGTGGCCGTTGATCGGG
917	TAATTCATGGGCTAGCCGAACCA
918	ACACTCTAAGCCGATTCCGTTCGA
919	GTGGGCGTGAGTGACACGCACAA A
920	ACGACTCCTCGGGCAAAGTACGTA
921	TGTGGTCATGGCGCTACTGTTTC
922	CTTCGCTAGCCAGAGCGGGTTCC
923	ACAGGGCGTGTAGCGTGTGACAA
924	GGTACTTCCGGCGTATCGGGCCAC
925	GTGGGTTTGTTCACCCCTCTGGG
926	ACGCAATTCCGCATTACTTACCG
927	CGCCTCGACTGCGGTCAAGCACAA
928	GTGAAATGGATCCAGAGAGGGCCA
929	TATAAACGCTGCAGGGCTCCGTTA
930	GTTATTCAAGCGGCTTGTAACGGG
931	GGGTTCTAGCGTGC CGTTCAGTT
932	TTGGGCTCGAGCGGTACACCACTA
933	CCGTCTTCAGGACAACGGTATGCG
934	GGACCCCTTGACAGATTGCGGCAC
935	TAAATTTATGCCAGGC GGCGCT
936	GCCGAACGCAAGATCGCTTGAAC T

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937	TAGGCCATTGGTCCCTAACGACGG
938	CAAACCACAGCTTACAGGCTGCGT
939	TAAACGGAGACTGGCACGGTAGCA
940	TAGCGCCATCACACTGGATCG
941	TGCTGACACAAACGAGCCGTTCG
942	CGCTTAACGGCATTGACTGTCCAC
943	TTCCACGGCCGTATTACGGATA
944	TTTATGCCGTTGCCGAGGAAGACT
945	AGTGCCGAGATAGGGACTGGCG
946	CTAGTCTCCACGCCCTCGGGACGA
947	CCGCCATTGGAAAGATGGATGATG
948	TGACGGTGAAAGTCGATTGCGAAG
949	ATATGCCGTACCAACCCGGTCCGA
950	CCATCAGTGAAGGGGTTGCTGCCA
951	CATATGTGCTGGCTTGCATGAC
952	TCTGCTTGGAAAGCCTGAACTGCT
953	CGATTTGGTCAAGAAGGCGGAAAT
954	ATCAGAGGCCTTCCGCCCTCGTTA
955	ATTGTTGTCGTTGCCACATCGCAG
956	TGAAAATGTGTCGACGCGAGTCT
957	GCGGGCGATGCTCCTAAAGGGTA
958	CCGCAATCTCATGCGTCGACCGT
959	TGCCCGCTAATCACCTGAACTTG
960	TTCCAGTAGCCAGCGGTAGTGTGA
961	CTGAATTCCGCCTATTGTTGGCA
962	GCTTGAACCTCGAGGGCGATGTTCT
963	CAAGCGTGGAAAGTACGACCCGCCA
964	GTGTGCACTGGATCCGAGCCCTAG
965	TCCCTGGGCTAGCATTGCGAGGTT
966	AGAACCAAAGACGCTTGGCG
967	CGTCACATGCAAACGTTCCCTCCC
968	TGACCGCATGTATTGAGTCGCT
969	GCGGGCCCAATGAGTATCCGTAT
970	TAGTGACTGTGAACGCCCTGGTT
971	GGCACCGTCTGCCGCGCGTATATC
972	TCGATGCAGTCTTTCCCGTCAA
973	ACCCCGTGGGTTTCGCCATTTT
974	CTACACCGCAGTTGTGACTTGTG
975	CGCAGCGACCTCATCTGGAGCC
976	CGACCCAGCACTCTAAATCGGT
977	ACGCGCCGCTCATCACTACAATCT
978	CGCAACTCCCTGTGGCAAAGCCAG

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979	TCGTTGGGCACATAAGGCAACTGA
980	CCGCTTGTAAATTGCCATTCTCCGT
981	GTAACCAGGGAGTCCTGGGCTGTG
982	AGCGCAAGATCTGGGGCAGTCAC
983	GCGTACATCTGCTCATCAGCATGG
984	CCTCTGTGGCAGGAAAGAAACCGT
985	CCTATGCAATGGACCTGCATCGGA
986	CTCGGTGGATGGCGAATAAGGATA
987	CCTCACTCGTGATGGCGTGACGCA
988	TACCGCTCACAGAACGCCATACGCC
989	CCGGAGAAGTTACGCCGATCGGAC
990	GCGCCCTCACTGCATTTTGGTAT
991	ACTTTCAGCACCGAACAGCGCAA
992	CTAAACGCCCTTGATGCATGAGCA
993	GCTTGCCCTTTACGATCGTCGCTA
994	CAGACATCGTACGCCACTCGGCATC
995	TAGCCCGCGCGCTCCTATGCTCTT
996	GATGCCCTTTGGTCCCCATGCCA
997	TGAGCTGCCCTGCCACGATGCCCTC
998	CCGCCGTATACTGCCATAGTTG
999	TAGTGCCTCCCGCGCTCATCCAAC
1000	CCCTAGATAAGTTGGGTGGGACG
1001	TGAAGGGCCACCTGATATGGTTTC
1002	GCCGCCTCCGACTGGTTAACCGGA
1003	CGCACGGCTACTAACAGCGGATCA
1004	CCGGACCAATTCCAACGAGGCATCG
1005	CATTGAGGTCCACCGTTACATCC
1006	AGGACGCAGCATGTCAGGCCGAG
1007	TAATCGCGGCCATACTACCAACG
1008	CGCAAATTCTCCGGCGGCAAGC
1009	GTGGCTCGACTAATGCCCTGGCGTG
1010	TGTGGCGTGTTCGGCTACTGT
1011	GTTCTCCCTTCTGCCGGTGGAA
1012	ACCTCGAGTCAGATTGTGCCCTT
1013	CAAGTGGACAGACGGTTGTTCCG
1014	TCCAGTTGAGTCGCGCCGACGAGG
1015	CGCAACAGGTCAGCCCTATTTC
1016	GCCGTGACTCCTGCAATGTCGGTA
1017	ATCAGCGCAAGCTGGCTGAAACA
1018	CCCTGGCCAGAACGAGAGGCCATG
1019	ACGATCAAGGACTCGTCAGGGTTG
1020	TTCATGGCACCAAGACCACCGTTA

1021	ACAGCAAGGAGATGGATTGCGACG
1022	CGTAAATATCTCGGGCGGTGTGAA
1023	GGAAACACGTGTTCGTCTGTTGGC
1024	CGATGTTAGGATTGGATAGGCCA
1025	ATCGGACAAGGACAAGTGGATGGT
1026	GCCCAGGAGAACAAAGTCGAGTTA
1027	AAATCCGACAAATGGGCACATGGA
1028	CAGTTAGGGATGCGGATGAGTGA
1029	CGGCAGGTGGAGATTCCGACATTG
1030	TAGGGCAGCCAGGTTCACTCATCT
1031	GCACCGTATTAGCAGTAGGCACGC
1032	ACGCATTACAGGTGTGCGAAGGGAA
1033	CGTGACTGCACGTGTTCCACAGGG
1034	GCTGAACCTACGCCCTAAATCGCG
1035	AGCACGCCAGGGAGGATCGAGTTA
1036	ATGAGGGCAAGGAATGGGTATGC
1037	GGGTCTCTCGTAATCAAAGGCCGA
1038	TATCTTGCACGCCCTCCATTAA
1039	GGTTACACCTACGGAATCCAGCGG
1040	ACACCGAGTTGGTCCGGTCAATAG
1041	TCCCAGATTAAACGCTAGCCACCG
1042	TTGGTAAAACGGCCCGTGGAAAG
1043	CCAGGGGAGTTGACAATGAGGCTG
1044	TCTGCCTTATTGGACCCTGGTCA
1045	TATGGGATGCTAAACCGGGTACA
1046	CACAGACGTCTGCGGGCTTGTGT
1047	AGAATGCCGTTGCCTACTCCCGT
1048	CGACGGATAATGCAGGCCCTCATGA
1049	ACCCCTAAAGCAATAGGTGGCG
1050	CACTCACGGCAGAACGCCCTGTTGT
1051	ATCAGCCCCACATATTCTGCCGT
1052	CAAATCTGGGTCGTCTAAACGC
1053	TGTCGCCCATGGCAGGTTAAATAC
1054	GGGGGCCCATCAATTATTATCGA
1055	GTCGAGCAGCTTGTATCGCGGG
1056	CCGCTAACGACCGAACGGCTCACAA
1057	TAGAATTAGCGAACGGTGATCCCG
1058	CACATGACATTGGCAAAGGTCCA
1059	TCAACGCACGGCGATGACTAGAT
1060	CGGGAAATGTCTTAGCCGTCGAA
1061	ATCAGAGCAAATCTGCAGCGGGGA
1062	GGCCTGTTCTGCCAACTGGGCT

	1063	ATTCACCTCGCTGATCGCTTCCG
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	1065	AGTTGTCTCATCCTGTCCGGGACC
	1066	CTTCTTGTGCACACTGCCAGGG
	1067	CACCTCATCGGAGCATAGCAACCC
	1068	ATGCGATCCCATGACAAGGGTTGCT
	1069	CCC GTGGAGATGATGTGGGCTTA
10	1070	CCCAATAGACGCCACAGCCAGTGA
	1071	AACGACCACGACCCCTGCCGAGTA
	1072	GGTGCTTGTCTGAGGCCAGTGAA
	1073	CTGTCGGCGCTGCTCTCCGAATT
	1074	CTCGCCGGAGTGTGTAAGCATTG
	1075	AGCAATCATGAGAGGTGGCCGGTG
15	1076	ATTTGCCACCGGGCAGAAAAAGAT
	1077	CCGCCCCGTGTTGGCATGTCTTTG
	1078	ATCGGAAGTGCTGACTGACACACG
	1079	CCTCAGACCCATCTGGGTTGACG
	1080	CTGTGTGGCTGGTCCGGCTGTC
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	1082	ACAGGCACGTAAGTGCTCAATCGG
	1083	AGCAAGATAGCGGGAGTGCCCCTA
	1084	GGTTTACGCCATGACATCCCGTCA
	1085	GTGCAGGCCTTTGTGTGAATCG
	1086	CTTCGAGGGTAGGGCTTCGAAACG
25	1087	AGTCGACACTTGGTTTACCAACGG
	1088	ACATAAATCTGCCCGCTGCACTC
	1089	GTTTGGTTTCCACGGAGGTTGA
	1090	GCAGGAACCAGATTAGTGTCCCAG
	1091	TTTGCTAGAGCGCGGAGCTAAAGC
30	1092	CTATGTGGCATCGCTGACATGCTC
	1093	CCTAAGTCGGTTGCAGCTGCTCT
	1094	GCGTTCGTCCACAGGAACGGAAGG
	1095	TAACCCCGCGCCCGAGAAATTGTCT
	1096	TATGGTGCTCAGAGCTGTTGCCAA
35	1097	TCATCGACCCACTAACGTCAAGGC
	1098	TGCTCAAGCTACCGCGTCACTCCC
	1099	AGCGGGAAGGTCTGAGGAGGGAAA
	1100	CCGATGTAGCACCAACGCAGTGGC
	1101	AAGTTCTGGGAATCACACGGCGCG
40	1102	CACCAACCTTACGTGCGCGTTAA
	1103	CGTTTCGGCTCCCTTCCGAATGC
	1104	GAGGAGGCCAATAGAGCAGCGCGC

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1105	AGTAATCTTGCAGGACACAAGCGG
1106	TGAGGACAAACCGCGCGTAGGATA
1107	TCGTAGAGACGCAGTGCCATCTC
1108	CGAAGCTACACCCCGAGTGCGGTG
1109	ATGATGTGATCTTCCATGGCTGG
1110	TGTACACGTATCGCGTCGCCAG
1111	GGTGTGCTTTACGCATGTACGCA
1112	AGGCAGGATACGTGGATGCTAGCC
1113	AAATTAGGCACAGCCCTCCCACAG
1114	ATAAGTTGGTGAGCCATTGCGA
1115	CCTATTCGGCGGACCTCGATGCC
1116	TTACCGGAATATGCACTGGCCGC
1117	CCTCTGGACGGTCCCTTGATCG
1118	CAAGCGAATGCTGTATTACGGCCT
1119	GCATTTCCCATGCCAGAACGTTGA
1120	GTTTGGCTAACCGTCCTGCCCTG
1121	AGGTTTGTCCGGCGAATGATGT
1122	ATGTCCACGAGTGCCTCGATATC
1123	AGACGCGTACGAGGGTTCTGCC
1124	AATACCGTTCCATCTGTGCGAGG
1125	ACACAAGGTGCCTCATCGAATGGT
1126	GCCGGCAAATCCTACAAAATCCA
1127	CTTATCCCATGTGCCGGTCTGACT
1128	GCAGGCCATAATGCATAGCACGGAA
1129	TACGGTGCATCGCAGTATGGTAA
1130	CACCAGATGTCGAGGATCATGCC
1131	GCTCCTACGCCAAAGAGGTATGG
1132	AGAATATGGGCAGCAGCAGCACTC
1133	CTGCAGTCGCACCGCAGTAGACCCG
1134	ATGTCCCTGACCGGAATTTCCA
1135	TTCGCCACGAGGCATTAGTCGAC
1136	ACGTGTTCCCGAGAATACGGTCT
1137	ATCCGCTGGCGCTTGACGAAGAA
1138	TGAACCAAATTCTACCGCGTGG
1139	CACGCGTAGGCTGGTGTGTCATT
1140	TCGATCCCGCGATCTGCCATTG
1141	GGAACACTCAACCAACCGTGGATCT
1142	TCACACACCAACTGCCACAGATG
1143	TGTGCTTAGGACACCAGGCAACCC
1144	GACATTAACCGACCGATTGTGC
1145	GGCACCGAGCCAGTAGGCCTCTGA
1146	CTCAAGCGTGCATGTTGGTAACCA

1147	AGGAAGGCCACCAACCAAAATTCG
1148	TTGGAGCCCTGACTGAACCAAATC
1149	TACGAACGCCAAGGTTATGCCAAT
1150	CGCACCAAGAGTTATGCAGGCTCAA
1151	CCAGCTTGGACGAGGAAGGATGTG
1152	GTCACGCCCTTCAAATGACCCACA
1153	TGCTAGACCCAGCCGAGTCTCGG
1154	TATTGTGGCACTTGGGTCCAGTGC
1155	CACGTGTGAGACCGGAAGTGCATC
1156	AACCTCCAGCAAAACGTCGAGGTT
1157	GGCAGCCTGATGCTACAGCACCGT
1158	CGGTCCGTCATCCTTCAGAGTTA
1159	CTATTGCGGACCCCTACGCAGTTT
1160	ACCTGTGCAGTCAGCACGAGTGC
1161	GAGAACACAGGTGGTCCACCC
1162	CCTCGCTAGAGAAATCCACGGGAT
1163	TAACATCGGTGCAAACCGTGGCGC
1164	ACCCAGAAGACATGGCATTCGCCT
1165	AAAAGCGCTGCTCTAACACCGCCG
1166	CAAGTCTGTCCATTCCCACCGT
1167	CCGACACATGGTGGGCTTTTAAG
1168	ACAGACCAGCTTTGCGCAGATT
1169	CGGCGATCCATTCACTCAAAGT
1170	GACGTTATCATGACACAGGTCGCG
1171	GGCAGAGTTGGATCGGATCCTCAA
1172	TTGCTGGCAAACAGCTCCTGAAGA
1173	CCTCAATGCCACCGAATTGGTAT
1174	GGAGTTAGCGTGATTAGTGC
1175	GAACCTGACGTGTCACGGAGGGT
1176	CACAAGCGACATTCTGGTCACG
1177	CCAGAATGCGTGAATTGCGTCCT
1178	CAAGGGAGCCCTCGAATTAGAGT
1179	ATTCTTGCTTCGGACGACTAGCCG
1180	TGCCACTTGATTCCAGATTGCC
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	1189	GGTCGAAATGAGCCAGCAGCAGAT
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	1192	AGGGTGA CTTCGAAGGTCCGA ACT
	1193	T CGTCCCCTCTGGTGGTCGAATCAC
	1194	T GTGCAAATTATGCTGGCGTGAG
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	1203	TTTCATGCCATATCGCCTCGCGCA
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	1206	GGTTAATGGAACGGCGTTAACGCG
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	1224	ACGACCGAGGTGA ACTTCGTGGAA
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	1226	CAGAGGGCAGATGTGACTCCTCAA
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	1237	ATGCGAGAGCAGAATTGAGCCGGT
	1238	AAGTTGGTCGTATTACGCGTGC
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	1240	CAACGGCGAAGACCCAGAATTAA
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	1242	ATGCATCCAGCGTCCCCTGATTA
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	1246	TGGTGTGAACTCCCTTGCCTGTT
	1247	TACTCCAGTCGCCTGCGCGCAAAC
	1248	CGCAATGCCGTAAGCATGCCAAGC
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	1324	GGACGACTCCGCAAAAAGGTCGT
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	1329	GGAATGTAGTCAAGGAGGACGGGG
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	1333	GGGTGATCTCTGAACGTCACCC
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	1338	TCGACGATAAAAGTGTCTCACGGAC
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	1347	ACTTCGGGAAAAAGGCTGGCATT
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	1352	AGTCACGCCAACGTCGGTTCTTT
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	1368	AGTTCTTGCCTGCACGAAACAGA
	1369	GCTCGCCGCGCGTCTTATGTCTG
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	1378	GGAGTGACCAAGCACAAGCATCGAG
	1379	TCGGACTGGAAGTAACTCGCATGA
	1380	GTAGGGTCAAGCACGATTGAAGCC
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	1382	GAATGACGCGCAGTGCATTGAAC
	1383	GTGCTCGTCAACCGCGGATAGAG
	1384	GC GGACCTGGGTTAATTGACGCGC
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	1394	TTCGTGGAGGGACTTGAGATCC
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	1529	CTTCGCAGGTTCGCAGACAATCC
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	1537	TCCGTCTCAGCCGCCCTCCCTATCC
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	1540	TTAGAAGCCGGTCTGGATTGCGT
	1541	TGCCGACCTTACCAAGGATCCTCG
	1542	GCCCACACTATAACCAAGCTGGCA
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	1544	CTTGCAGTTATGCTGACCGTCC
	1545	TGCCTCAAATTACTTACCGCCGT
	1546	CCCGTATGCCGAAGCTATGGCTA
	1547	TCGTTCAACCCCCACACTTCAGTTG
	1548	CAATGTGGGGGACATTCAAGGTT
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	1552	GGCTTGCTCTCGTTTGATTGCA
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	1557	CAGCCCGAAAGGAAAGCCTCCGTG
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	1560	TGAGGGAGAACCGAAATCTGCTT
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	1589	GCCCTCGACGAACTCATCCTGAAC
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	1593	GCTTCGAGTCGGTGGCATCTGTAT
	1594	GGTCTGGGCCATCGACTTGCTGC
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	1599	TCCTATTGACCGTGCATCGTGATC
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	1602	GTGCCATTGCCACCCATAATGCGT
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	1604	TCCGATGGGAGAGGGCTGATCTCAC
	1605	CACTACTGAAGTGGCCTGGCGCTG
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1624	GGCCAACATTTCTAGGGGAGTGCC
1625	TTCTTCGGGATTGTCCCTCACC
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	1656	CGACAGTTCCGTCCGTCTTGAGGA
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	1660	GTGTGGAAGATGCAATTGGAACGG
	1661	ATACAACGGTAGGTGACAGGGCG
	1662	GCCGTGGGAGTAAGGGTACAAAGG
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	1665	CATGCCTGAACAATCTGCATCCC
	1666	GAGCCTGGCTCCACAGCTGTGCTC
	1667	CTTTCGATAACCATCGTTGGCGATC
	1668	CCCGGAGGTGAGGCATTGAATATG
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	1670	GAAATGCCCTGGGGACTTTTGCC
	1671	TTTGCCTTCACAACAGACGCAGCA
	1672	AAATCCAAGACGTCGGGCGTAT
	1673	CAACGGCGGTAGCTAAACCGTAA
	1674	GGCCAACGACAATGCGAAACCTTC
25	1675	GACATCACGAAAATCTCAGCGCA
	1676	ACGTTCCGTCCACAACCGTATGTT
	1677	GCTCATAGGTCTCCGTAGCCGT
	1678	GAAACGAGTCTCGCGCCCTAGA
	1679	CGGGACAGAAGCAAGTTACATCGG
30	1680	TGACCGCTCGATAACCAGGAGGGTG
	1681	CTGGCAATAAGACCTCCGACCA
	1682	TGCGCGACGTATGTTGGTGATTA
	1683	GTTGGTTGTGGAACACACCCGCT
	1684	TGTGGGTTCGGAAACACAGGAAGT
35	1685	GGAAAAAACGGCAATTAGCCGAGT
	1686	TGGTGCGGAGTGCCCTCTATTGGG
	1687	AACCAACAGGCTGCAGCCCAGACT
	1688	AAACAGATCCATCTGCACGCCAGG
	1689	GGAATACCGCGGGGATTATGGCTT
40	1690	TACTGTTCGCGGCAAACCGTCACT
	1691	GATCTCTCGTGGAGCACGTTTCC
	1692	GGCATAGCAAACCTTGACCTCAA

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1693	ATCTGGGATTCGCGAGCCAATATC
1694	CGATCAGGATATCATTACGCCCG
1695	ACGGTACCGAAACGGTCTCAGCGT
1696	CTCCCATACTGCCTTCTTACCGA
1697	GCACGAGAACCTAATTGTCGCACA
1698	GCCACACGATCAAGACAGCCGATG
1699	CCCGTTAACTCACGAGCGGTCAAT
1700	AGAGAAGGTCAATTGCCTGTCGGTG
1701	CGGGCCCTCTTAAAGTAGAGCAGG
1702	ACATCGCGTCCGAGGGAGTTAGCG
1703	AATGCCTAATCGAGCCAGCGGATC
1704	CTCGATCTTTAAACCAGCGCTT
1705	CGTTCCTGGAAGGCAGGGTCTCAC
1706	CCTGTGCTTACTATCGCGATCCA
1707	GTTAGTCGCCCTATTGGCCTGGTT
1708	CCGGTGAGATGACTGTAAATGCCA
1709	CGTGGTTAAAACATCGCGCTTCG
1710	TAAGACCGAGAACATGGGTCCAC
1711	CACCACAGCTTCTTGTTCGACCC
1712	TCGGGTCCGTACCACCACTTTGC
1713	CCAAGCCCCGAGTACCGAAGATTT
1714	TCCGTGATATGGTCGTGGCGCGGT
1715	TGTCTGTGTCATGGCACCTCGCAT
1716	AGGACTGCAGTGTGACGTCTGAT
1717	CCATCCTCATGTACAGCGCCGCTG
1718	GTACCCGCGCTTCCTCGACACAG
1719	ACGGGTCTGGTCGACTAAGGCTT
1720	CGTATCGAAGGCGTGTACAACCGG
1721	TGCCCCGCCCTTATGCAACGCTCA
1722	AAACTTACGAGACGGCGGCTGCCA
1723	AAGTCTGACAAACGGAACGGGTGT
1724	TAAGCGCAGACCAAAAGTATGCGGC
1725	GCAGTTTTCAGATCCTCCGCAA
1726	TCGGAAGCATTACGCGATCTCAG
1727	CACAGAACGGTTGAACGAACGCC
1728	GCATGCTCAGATGGTCGTGCTCAC
1729	AAGGATTCTCGCTTCCGGCATGAT
1730	GGTGGGGTAGCGCTGGTATGAAAA
1731	ATTATTACGGGACCGAACCAACGG
1732	GCGCGAGTGTATGATGTTACGT
1733	GACATTGCGACTTGGTCGTCCGC
1734	TCATTAGTGCAGGCACCGATCAAG

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1735	GAGTTGTGCGGAGTCATCGGAGTC
1736	GCCTTACAGATTGGCGGGCTAT
1737	ATGGCGTTGCGAAGTCGATACAG
1738	TGCATCGGCCTCAATCAGAGAACT
1739	ACAATCATGGCAATCTGGCAAATG
1740	GACGTGGAAGAGTGCAGATCAGCA
1741	AGGGCAGGGGACGGACAGTAAGTC
1742	GCATAGGGCGAATCTAGTACGGGC
1743	TCCGGCGCATCCTCATTAGCAACT
1744	TGGCCGCTTCCACTAATATTGGAC
1745	CCGGCGGACGGCTTTGTCAATGA
1746	CGAGCAACCCAAAAGGAAGCAGTA
1747	GCGTATGATTGGCAATCCGCCAG
1748	AGTACCGCTACAACGCTGGTCGC
1749	GGGCAGGCCAGGTCCACCTGAGAA
1750	CCACTTCTGTGACCGAACCGTGCT
1751	CCTGGTACCAGGCAGCAGTTGATT
1752	TTAGGGTACCGTCGAGAGACGCCA
1753	GGTTGCTTGTGCCGTGAGGTAGT
1754	TGCTTCGACCGATGAAACTCGAAG
1755	TGCCACCCATACTATGCCAGTGG
1756	TGTGCGGCAACCGCGTGAAGACGTT
1757	TGAGAGAAGCTGCCCTCGGATCAG
1758	TATTGCGAATTGAGTACGTGCC
1759	CGAGAGGGGTTCCCCAGTGATCGA
1760	TGCCTGGGTGTCGTTCTAATTCT
1761	GTGCGTCATTGGGTATCCAA
1762	AGGGCTCCCAGCATAACCGTTG
1763	AACTAGCCGCACCTTGTGCAGAG
1764	TTAGCCCAGCCCTCAATGGGAAC
1765	CGGCCTCGGTTGACGGTAGTCT
1766	TCTTGAGGCGCGGACCCGCATAT
1767	GATGGTTGCCCTTGTGTCGCAGC
1768	GAGATTCAATACAGGCCGCCGGTC
1769	AGGGCGAAGGAAGGTTCCGTTTT
1770	CTCGACCCCTGCCACTACTGGTC
1771	TGTTCCGCGGTCTACGCATTACTG
1772	GAGACGACGTCCCTACACCCGCTAA
1773	AGATTGCGACAGCGACACGTGATT
1774	GATACCGTTGGCATTCTCGGTA
1775	GATTGGGAGGCATTCAAGCGACGGA
1776	AGGAGGAAACGAGGGCGTAGGTT

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1777	GCCAAACAACGTCGTGACGCCTAGC
1778	TTTAATGCGGAAAGGGATGCACGCG
1779	TTATCGGCCGTTAAAATGGGATGG
1780	CCTTGGATTGTTCATCGCTAGCA
1781	AAGTGAACGTCAGTGGTCTTCGA
1782	TCCTTACCCCTCGTTCAAACGCCT
1783	ATT CCTGAACC ATGCATGGCCTGT
1784	AGCGAGACGCTCGATCACGAAC TA
1785	GCTGGTCTGGCTCGCTGTTAGAA
1786	CGTGC CGGGCAT AAAGATA GG TCT
1787	TCTGGCACTCACATCGGACAGTCT
1788	ACC ATTGGAGGACCACAGAGCTCC
1789	TCCAGGGT CGGAGTACATGGCGGG
1790	ATATGCCGTCGGATCGTACACGCA
1791	TGCTGGCGTCAACACTTCCC GATT
1792	CAGGGCGGTGC GGGTGA ACTAGCCA
1793	CATGGACTGCCGTACATCAGCTGG
1794	CCGGCCATACGCTGGCAAGATTAC
1795	AGCGGACACCTGTACTCTCCTCCA
1796	GGAGCCACACCAGTCGAAGATGGT
1797	CGCCACCGGAAATTGAAAAGACTG
1798	TGAAACGGATGTTGCTTCTTGACG
1799	TTGAAGCGGTGAAGAGCCTGTCCT
1800	CGAACCAAGCTGCATTGTCA GTGG
1801	GAGTCTGCGCTTGCAATCTTGCG
1802	GCTGGGTATAGTTGCCTGGCAATG
1803	GCAGGGCGTTCCATATT CGCAACCC
1804	GCGCCAACTAATACCTCCACCGCG
1805	TGGCGTTCA GTGCAACGCTGGTTA
1806	CAAAACTGACGGGTATGGGAGCGC
1807	AGGTGTGCGCTGGAACCCGACTTGT
1808	CTTCCAAAAGCGCAATTGGCTTTG
1809	TCGGGCTTCTCGCAATTCTGTCA G
1810	GCCAAAAGAATCGCCTGGTAGGT
1811	TGGTCCCCGCACCGAGAGACTGTA
1812	CGAGGCCGTAGTGGGGACTGCTCT
1813	CGATCTGCCATAGAGGGGACTTT
1814	TGTGCAATCGGCCTTCTCAGAGCC
1815	GATCACCTGGACCGCTACCGTTT
1816	ATGGGGAGTTAAGGACCC TGCA CC
1817	CATTGTGGACAGCCAATGGTGGCT
1818	CCATCACCATGCCACGGTAAGATC

	1819	GCACCCGTGTCGGTGGTTAGCAAG
5	1820	GGAGTGGGTTCCCGGAATTCACTG
	1821	GGGGATTCCTTCGCAGGCTCGA
	1822	CATTGATCATGTGCACTTGCACCA
	1823	AGCAGCGCTGCGCTTGGAT
	1824	CGAGTAACCGGGTTGCGAA
	1825	TGGCCTGGAACATAGGTGGAACTC
10	1826	CGCACACCAAGCGTTATTGAGAA
	1827	TCACCTTCACAGTGGGCATACAGC
	1828	CAAATATCCCTGAGCCCTCGAGCT
	1829	GGGAGCTGGTGAGCAGATGTAACG
	1830	AGGATTGCTTTCGCTTATGCGGA
	1831	ATCGTTGGCGCTACGCAATTGT
15	1832	CCGATTGGTCCCAAATGCAACGTT
	1833	AAGGGTCAAGCTCATGGAGCGAA
	1834	TCTGACGTGTTCAAGGGCTCGCT
	1835	CGCACCACTCCGAGGTATTTGTCT
	1836	AAGGGGTAAAAAGGAGAACCGA
20	1837	AAACCACGCAAATGGCGATAACCAT
	1838	CAGAAGGGATGACGCCCTAACGTCG
	1839	CATGACGAGAGCGGACCTGAAGTG
	1840	CTGGACATGTTGTTGCCACTG
	1841	AAGACCGACTCTCGTCGTTGCAC
	1842	GCGCGATTACATACCGTTCCGTA
25	1843	CACTGACCGGACCAACCTAACAT
	1844	AGTGCAAGTCTAGACACGCCGAG
	1845	GGTTGGTGCAGAGATCCTGGACTGT
	1846	GGTCGTCCCGAAACGTAAACGAGG
30	1847	GAATAGTACGATCACGGGGCGGGT
	1848	CCGACCTGACCCCTGTGTACAGGTT
	1849	TGCTCACTGCCACACTGTTATGG
	1850	CGAGGAAACACATTCTTGGGCC
	1851	TGGCACCGGGTGGATTCTGTCTA
35	1852	GAGGCACGGTGTAGTGGTTGTGC
	1853	ATGCAGATGGATCTTTGCACGC
	1854	TGCGATAGCCAAGAGTCGAGGAC
	1855	ATGGCGTGTCAAGCGAACTGCCTGG
	1856	CAATGCAGCTCGGAAGTCAGGTG
	1857	AGGATCAGTGCACATGTCCCCCTCA
40	1858	CACATCTGGCTGTCAACCGAGAA
	1859	CGCATTATCACCTCAATGCCAGTG
	1860	ACATCCGCAGACTCCCTATAGCCC

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1861	GTGAACCCGAAACGAGGGGAGTCTC
1862	GCGTAGGGAATTGCCTCACGACT
1863	TTTACCGCGTCGCTCGGTTAGTG
1864	GAGAGGCGTAGGCCGGTTAGC
1865	GCATGCTGATAACGAATGCTTCCC
1866	CTGAAGCTCGTGTGCGATGAGGGA
1867	ACAACGGCATGAGGAGGCTTTTC
1868	TTTGGAGACGCCAGTACCGCGGT
1869	GCTATCATTGGTGTAAAGCCGCC
1870	TCAACATCCAGGGCGGTGCTTGGT
1871	TTCGATGTAATCCCCAAAGATGCC
1872	GGACCTTCGGCAGGTTATGCCGT
1873	AGTAAGAAGAGGCAGGCCACCT
1874	AACGGCTCCCCGTGACTGCTTA
1875	CCTATACCCTCGTGGTCCACGTT
1876	CCGCGCAGGCGCTAACACTCAAGG
1877	AAATGGGCCAGTCAAATCCTTGGT
1878	ACGGTTTGAATACTGCTGGCAG
1879	CCGCTTGAGGTTCAAGTCAGAGCT
1880	ATCGTCCCCGAAGACACTAAACG
1881	ACCTGAACCAGGGGATTGCTTTA
1882	ACCCCTATACGCTGGGCTAACGGG
1883	TGTTTCGCGACTAGAAGCCTTGC
1884	GAAGTTGGCGGCTCACCGTATTAA
1885	TGGCTACACCGCTTAGGAGGAACC
1886	CCACAGTTGCGTGAATTACATCGC
1887	ACTGCCACTGCGTCTGAAGAGTGG
1888	GCGCCAGCAAATTCTGTGTGGTGT
1889	TGCCTCCGTCGAGCCGAATAGCCA
1890	GTACAAACGGCGCTATTCGTCC
1891	GCTTCCCTGGCTCTGAACGGAAAC
1892	CGGCTACCCAGGCAGATAAGCTGA
1893	GGTTGGACCCGACAGGGAAATTCC
1894	GGGAATAACCGCGCTTGTAAATA
1895	TGGTTCGGTGAGGTTATGTTCGGT
1896	TCGGTAGGGTTCACTCGCTGAGGA
1897	TTCGGAGTGTGCCGGTGCTAGTAC
1898	TCGTACTGGAATGATGGCCGGGCC
1899	TCCGTCGACCGTCCAGCGAAGTTT
1900	AGGGAATATAACAAACACCGCGCAC
1901	ATGTCCCAGGAAACCAAGCTACCTCA
1902	ACCAGCGACTTAGATAGCCGTCCG

1903	GGAAAACCTCCTTGCCTCAACCA
1904	ACGTGCGTCATACCCAAAGAGGAC
1905	ACGCCACTTCCCTAGAACCAACG
1906	CGAAGTACGCAATAGTGCACCCCT
1907	GATCCCAGGCGATCACCTATCAAT
1908	AGAAAGCGACCGTTTCAGGCTAGC
1909	CGCTCCCTTCATAGTCCTCTCCG
1910	GTGGGTGGTCATAACGACAGCAGA
1911	CTGGAGGCTGCATCGTCGTAACA
1912	CACCATGAGTTCGGAGCGAGGAT
1913	CAAGCTGCCTTCGATGAGAGATTG
1914	CCTGGGAGCAATGACCGCTCTGGT
1915	TCCGGCGCTTACCAAGATGAGAC
1916	CGACCGCGTCGCGTATACTATCCG
1917	AACATTGCTAGTGGGTCCAACA
1918	TGTATGATCATCCGACCGAGCAGC
1919	AGTGCGCCGAGAGGGTGAATAGAC
1920	AGGCTTGTCTGGACCAGCACCAC
1921	GGGGCCACATAAAGAATTCCGAAC
1922	TGGTGAAAGATAATCCGATGGCA
1923	ATTTCCACCAACGCTCTGCCAAAT
1924	CGCGTAAAGCTGTCACCGATGACC
1925	TCCCCAACCGTAACAAACAGCGAC
1926	CCTCTGCTCGCCTTACACCCATGG
1927	CAAGCTGCTCCTGTGCTGAAGGGC
1928	AAACGAACGATGGTCGGTAGACCG
1929	TCAGTTGATGGCTATTGCCCTC
1930	GGCTCTAACGGACGCAAATCATA
1931	AGTAGAGTGTGCGGCTGCCGATC
1932	AGACACTAGACCGCCGTGACCTGA
1933	ACCGAGCACCGAACCTTGCTGTCC
1934	CCGTGGCCAAGATAACGAACGAATT
1935	CCTCCTACAGCATCCACATGAGGG
1936	CACTCGGCAAATACGTATGCGCAT
1937	ACCGAGTTGAAGCACGAATTGGG
1938	GACCACCTCGGAAGATCGTTCTGC
1939	TCAACTGGCAAAACGAAGAGCACA
1940	GCTTAGCCTCACACGTGCATACCA
1941	CTGCGGTCTCCAAGTACCAATTG
1942	GTTCCGTATTACGGCGGCCATAAG
1943	ATCGACGCAACCGGATAGTCTCTG
1944	CGCAGATAAACCGGCATTTCAAG

	1945	ACCTGCCAATACGGGTCTACGGTT
5	1946	ACACCTGTTGCCATGCTGATCCGT
	1947	AAACTGTCTACTGCGCAATTCCGC
	1948	GCAACTAGCCCCTGCTAGGATCGT
	1949	TCGTAGTGGTGGATTGTTGTCGT
	1950	GGCTTACTCCTCAATTGCGACACG
0	1951	CACGACTCCCTGCCAGATTGATT
	1952	CTTAGACGTCGGCAATGTACGTC
	1953	CTCAGAGCACAATCTGCCCTGCCT
	1954	GCTAGGAAAGTCGGCATTCATGGG
	1955	AAAGCCCCAAAATCCGCCCTAAC
	1956	GCGCAACGCTAAGGGACTATCAAG
	1957	CGTCCGCTGGGATGAGTCTCCTGC
15	1958	ACAGGCCTCGTATTGGTGTGGGT
	1959	CATTCTCCTTCCGGGACCACGCC
	1960	TGGAGTTGACCAAGCTCAGTGC
	1961	ACGCGCCACTGCAATTGCAAACAC
	1962	AGTTCATGGAGCCGGCGTATTGTT
	1963	ACGTTTAATGCGGGGCCGCCTAC
20	1964	TGAGGGCTTACGCTACGCGCAGGT
	1965	CAGCGTTATGAGCGCGGAGTTAT
	1966	GTCCACGTGACCACGGATAGTTGG
	1967	GATTATGCTCCTACGCCCTGCTCCG
	1968	TCGTCAAGGGCATGATGTGGGA
25	1969	GATGGACCGCCAAGACACCTTGA
	1970	TACACGAGGATGGGTCAAGCTTT
	1971	ACACGCACAAACGTTGAAAGGC
	1972	GTTATCGTGGGCCGATGGTACTGA
	1973	ACATGACCGTATCCGCCTGCTTCG
30	1974	GAAGGCGAACCACTGAAACTACGC
	1975	TGACTTTGCAACGGGTGGAACCA
	1976	TGAATTCGTAGGTTGGTGCGG
	1977	AGCATTATGAAGCGGCCATTGCG
	1978	TGCTCCCTCGCTGGTACCGTGAG
35	1979	CGCAGCAAGAACAGCAACTGTTG
	1980	AGACGCTTGGAGTGAAACTCGGA
	1981	CATTCGTAGAATGCCCAAATGGA
	1982	CCAGAAGGTTGGGACCCGTCGTG
	1983	GAGAAGCCGGTCTCAGAGCACAT
40	1984	TTGCGTTGCAAGATATCTGGCCCG
	1985	GGGTTGCATGTTCAAGGCAAGACGA
	1986	CTCACGAAGGTGACATATCACGCC

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1987	GCCCCGAGATAACGGGTTCAAAAAGA
1988	CATCTTCGCGCTTCTTCACTCCGC
1989	TTACACGGTAAGCGTACGGCCGCC
1990	ACCTTCGGACAATGTGGCGTTCGC
1991	TGAATGGTTCTGCTAGGCCCACAC
1992	CACGCCCTGTCTGACATATGGATGC
1993	CGCCTCAACCCAATCTGAGAACGT
1994	TTACGCTTACTGCGAGCTGGGTCC
1995	GGCTTGTTGGGCAATACGCATCTT
1996	CACTCTCCTTGGATGCGGAACAA
1997	CTTCGAAGCACTTCAGACTTGGGC
1998	GACCAGCCATCACGTAACGGCCCT
1999	AGGAACCGGATGTGGTTATGGAGC
2000	ATCCATGGGCAACTGAGCCTATGC
2001	GGAACAGCACTTGTACCGCCCCAC
2002	TGGCTCGCTTCAAGCCTGTTGCT
2003	CAAACGTGAGGTATGACCACCAT
2004	ACCGATGTCTTGAAGTCCGGAGGT
2005	CGAAAATGCATGATGATCTCCCT
2006	TTTGGTATTCTCGCTGCACCGTTG
2007	GCGTACTCAACCACATTCCCGACC
2008	AGCAAACAAACAGCGGTCCGAGCAT
2009	GGACTAGGAGCAGGGATAGCTGAG
2010	CCTTAACGAAAACCTGTCGACCGC
2011	CTCGATCGCATAAGCAAGAAACCG
2012	CCCGTTGTTGGCGACAAAAAGT
2013	CGGC GGCTCTCGCATGATCTCGTT
2014	CGGATGGAGAGGAGTCTACGTCCC
2015	ACCAAATCAGACTAGCGACTGCGG
2016	CAGAACAAATATCGTGCCTAACCG
2017	CCTTGCGCGCTCCGAGTAAGGTA
2018	GGAAACGGCACCTATCTGCGTGA
2019	CGACCGACAAACCAATGCCGCC
2020	CCAAGGGTGTGGAGCTGAAGAGA
2021	TTAAGTGCATAGTCCTCGTGGG
2022	GCCTGGTGGGTAAGTCATGATGC
2023	GAGCAGCAGATTGATGCGCTTATG
2024	TGCGCCAACCTCCGGAATATTGCG
2025	AACCCCATCATGAAATGCTCTCCG
2026	GTCCAACGGTACTGGCGTGATGTT
2027	ACTCGGCTGATCGTGAGATGGTGA
2028	ATTCGTGGCGCATCTCGGAATGT

	2029	TCCCGTCCGTAAATCCAGGGAAACA
	2030	CTTCGCTGCACCTACATTGCCCA
	2031	GCGTGTAGATGACTGTGCTTG
	2032	CTATGGTATCGAGACATCGGCCGA
	2033	CCTCGTACTCCGTGTATGCACAA
	2034	TGGTGCCTCCGTAGTGCCTGCACT
	2035	CGCGATCCTAGTTGAAAGCTTGC
	2036	ACGATCCAGGTGTTGGGACTAAG
0	2037	CCAATCTAGGATAACACCACGCCCG
	2038	GATACGTGGGGTATAGGCAGGCC
	2039	CATGGAACAAACCGTCGTAGGGGA
	2040	ACACTCGCGCAGTATTGAGTCGT
	2041	CTCAGTCTCGAAGGTGATCCGACC
	2042	TCCCAATCCCCGTGGTATCGTCGT
5	2043	AATCAACGTAGTCCGGTGGTCCG
	2044	CTTAACAACCCAGGGGTTGGCT
	2045	CCATCCTGAGAGTGACGGAGGTGC
	2046	CTACCGCTGCATGGCGTTAGATTG
	2047	TTATTGGTGGCGGACGGAGTGAGT
20	2048	TTAAGGGTGAACTAACCGCGTGA
	2049	TTTGATTGAAACGCTGCGCACTAC
	2050	TCATGTGTAGGTGCGGGCCGTAC
	2051	CTCCGAACCTTCTGGCCTCTTT
	2052	CTGTTGCCCATGGCCCCGACACTC
25	2053	CACGATCGCTGAGAACACATCAC
	2054	CGGATCATAAGCGTCCGCCCTCGT
	2055	AGGTTAACGCAACATGTGATCCGC
	2056	GGGAAAAACAGCTAACGCCTGCGA
	2057	ACTTATTGCCGGATCCGTACACA
30	2058	TGCGGTCTGGAAAGGAAGGGAGGG
	2059	GCTGCCACCTGGACATCGCATACA
	2060	GCAGGCATGACAGTGGCGTAGTAC
	2061	GCGGCCCTGATGGTTGGCTGAGC
	2062	TCCCCATTAGTCCCCTCCATCAC
35	2063	GCAACACAAATGCGAGCGTAGGAG
	2064	GGCGTTGTATTGAGCCACGTAG
	2065	GGTAACGTGACGTGGAATTCCG
	2066	ACTTCACAAACGCTCCGTTGGACAC
	2067	CCGAATTATAAGCGCAAGGCACA
40	2068	GGACCCGATAAGACTCTGACGCCG
	2069	ACCCGTTCTCGTAGGAACCTGCT
	2070	CACGTTGACTGTATCTGGTTGCC

	2071	CCTCGGATGGGCCCATGACCTTGA
5	2072	GGACGCCTGCTGTAGGGGTTGAT
	2073	CTCGAGCGTGGGCTAAAAGAGCAT
	2074	TTTACTCTTAGGGCGCGTTGGG
	2075	ACCACCAACATAGCGCGCACTAGT
	2076	TGGTTACACGGCAGCCCAGCGTAAG
	2077	TTATGGTACGTTGCTGCGTGCAGG
0	2078	ACCGCGGATCTAACGAATCCCATT
	2079	CATGATCCCAGCCCTTAGGTTAACG
	2080	TACCGCTCAAAGGGTTGCCGAAT
	2081	GCACCGCGTCAATATTACCGAGGA
	2082	GTGTCGCGGCTTACAGAAGGAGA
	2083	GCAAGCCATACCGCAATAAACTCG
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	2085	CGAGACTAGTGCGATGCAGGGTA
	2086	GCCTCATCATAGACGCTGGATGCA
	2087	GACAGGCGTCGGAAGCTCTCAAG
	2088	GCTACGAATCTTCCCTGTCGCCAC
	2089	TTGGCAGAACGTACCAAGTGGGT
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	2091	TCATGAACCTTCTGATGCCCGAA
	2092	CGCCGCATTACCTAAAAACGTGC
	2093	ACGAGTCCAACCGCCTCATTGATT
	2094	GCGAAGAGTTGCTACTTCCGCC
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	2096	AATCCTGTGCACCCGTGAGACGCG
	2097	AACCTATATGCATCACCGCAGGCC
	2098	GAACTTGGCAAAACAGCCGGAAA
	2099	CTCTATGGCCGTTGCCGTCTGCA
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	2101	CCTGGCTTTCACACGCCAAGAAA
	2102	CACTCAGCGTAGCCTGAAGCCTGG
	2103	GAATTATCGACCGCAGCGGTGCG
	2104	GTGACATCACATGGTGGCCGAGCG
35	2105	AGCACCTTGCCGAGTCACCAAGTGA
	2106	TAGGTTGCAGGAATGGTGGCACC
	2107	GTCCCATACGTGGTACCGGGAT
	2108	TCGGATACTCTCGCGTGCCACGGG
	2109	CAACGTTGCCCTAACGCCAAAT
40	2110	GTTAGGTCACCGGGCATATCCTA
	2111	GTTCACCGGCCTCTACTTGGGTTT
	2112	AATCCCGCGTCTAGGTATGTGGTC

	2113	GCTACGCCCTGGAGGTGGTACCC
5	2114	CAGGGAATGCTACAAAGGGTCCAA
	2115	AAGGGTTAGCTGCCCGGTTAACAG
	2116	CCTCGCAAGCGCATAATTATGCC
	2117	GCCTCCCGTCATGGTCAAGGGAA
10	2118	GCTGTTAGCGGGCACCTGTGCAC
	2119	CGCTGACTTAGCTCTGATGTGCCG
	2120	TTCATGGCATTCATCACGAAGGAA
	2121	TAGTGTTATGCCCGTGTGAATG
15	2122	CATGTAAGGGCACGGTCGTGGCA
	2123	CAGGAAGCTCGCTCCGTGATGCAC
	2124	CCTGCTGATAGCAACCTCACTGCA
	2125	ACTACGAGGGGCAGGGTCTAGGCG
	2126	CATAATGTGGGTGCTGACGCCGAT
20	2127	TAGCGAATCCACACAGAGCCGCTC
	2128	TCGCGAAATCCCTAAATCCTGTGC
	2129	TGGCACGAATCAAGCCACCAACTC
	2130	CGGGACCGTCTTGCTATCTGACG
	2131	AGGCCCGCCTTGTATTGGTCAT
25	2132	CTGGTCCCATA CGCCGCTGACTAG
	2133	TGCTAACTCGGGCCCTACAGAGTC
	2134	TGGTTTTATGTTGGTAGCGTCCG
	2135	AGCTCAAACCTCTCCCACGGGATG
	2136	CGCGAAGATAGTGAATCCGCATC
	2137	GAGTGAAACCTCTCGCGGGTTGCA
	2138	TCGAATGCTCTGCAGTGACGTCAA
	2139	AGGTGGCAATGATCGACGACCCCTG
	2140	ACCTAACACAGCCGACCAGGTGA
30	2141	GTCCGGAGCCGTGCAAAGCAATAA
	2142	TCTGCCTGACTGCTACATGCTCCC
	2143	CTTTGGGGATTAGAGGCCGACAA
	2144	GGCATAAAGGCTTCCGTTCTGTC
	2145	CGGGACCGTAAAGCGGGCAGATAG
35	2146	TTTCAAGAGTGCATCGAACCCACG
	2147	CCGGCATCCCTCTCGCTGTTGCC
	2148	ACACAGAGACGCGAACGGAGTGCA
	2149	AGCGGCATTCTCCCACTCGTTACT
	2150	GGAGCGTACTCGCCCTCGCAAGTC
	2151	AAACCCGAATGACACGGCAGATAA
40	2152	GGTCGGGTCCATATCCAAGTAGGG
	2153	AACCAGCGGATCGATAAAACGACA
	2154	GGTGTCCACCCGTTAACGCCGGTA

2155	AGCGCGACGTGGCTGGCGTAAA
2156	TCCCACGGCTATAGGTCCAACGAC
2157	ATCAACGAACGATGCCGTTAGGTG
2158	GAGGCTAAGCCGTATGGCCGAGGC
2159	ACGGTCCGAAATGGTAGAGGCAC
2160	ACGCAAACCATTCCCTCGAGTAGGC
2161	TTACACGCTCGCTATTGGGCCATA
2162	CTCGGCACGGGTTAGAACGCCGG
2163	ATTCGGTAAAGGTATCGGGCTAGCG
2164	AGCACACCGTTATACATGACGGCG
2165	AGTCCTGCCGTTCGCTATGGAA
2166	GGGCTTATGACCAGTCAGGTTGGA
2167	GGTCACCACACGAGTGCCTGGTCT
2168	TTGATCGTGTCTCCGAAACCCCTC
2169	ATTGTCGGCATCGGCATTCTTAA
2170	GGGTCCAACGACTTCTCGCTGCTG
2171	CAAATTCTGGGGGCCATAGTGG
2172	CCAGAGTATCCGCCGTAGACGGT
2173	TCCTGCAGATCATCTCGTGTCTGG
2174	TGCGGGAGATTTGAACAAGCTGTA
2175	TTAGACGCCGAGCTAGGCAACGTC
2176	TTTCGGCAGAACATCTCGATTCAAC
2177	TGGCGAGCAGACCTACAAGACAGA
2178	GGCGACAGACCGGTACATCGGCCA
2179	TCTAGACCTCGTTCGTGGACC
2180	GCCGAGCGTGGTACCATACGTTCA
2181	TAATCACACCCGCTTCTGTGGCT
2182	GGCCGGAGCCATTGGACACTTCTT
2183	CCTGTAGACCTGCATGGATCGCTG
2184	GTGTGTGTCTCGCTGGGCAC
2185	ATCGCCGTTCCCGAAAATAAGCA
2186	TGGATCAACGGGTAGTGAAAACG
2187	AAGCGACGATGCTTCTTGAGCTG
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2189	ACGGGCTGGACAAGAGCTAGAAA
2190	GGTAACTGGCTCCGCTCTCACATC
2191	ACTCTGGCTGGCGAACGTGAC
2192	GACCGAGGACCAGTCCTGCTC
2193	AGTAGCTCTGGCGCTAACGGCA
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2195	TTAGCAGGGAGGTTGTCGGCTCAT
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2197	AGAACGTGGATTGTACGCTCCGCC
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2205	GCGTGGAAATAACGCCCTAGTTCA
2206	GGTCTACCATTTCTGGCCCACCG
2207	ACACCTCTCTGGCGTAGACGCTCA
2208	GTAGAGGGTGCAGGACTCGTCGC
2209	GTAAGCAGGAGGCGAAGGCGCGAA
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2211	AACCTGATTCAGGGTCAGCCCGA
2212	GTCACGCGATTGGCCCACCTATTAA
2213	ACGATGCCGCGCATGTAACCTAGT
2214	TGAGAGATGTCTCGTCAACGCCCTG
2215	GCATATCTCGCGGTGACAGACGAA
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2217	GACCCAACGTCGAAATTGTGCGAT
2218	TGAAAATCGGGGCATCTAGTTGG
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2220	CATTCCATTATCCGCAGTCGCT
2221	CCTGTCTGTCGAGCCAGCGTCTAT
2222	TCAGCGCGCTAAACAAGTTATGC
2223	ACGCCTACGAACGCCAACAGAGAG
2224	TGCGCATCTACCATTTGTGTGGATC
2225	AAGTCCCGCGCTCGCTCCTGTAATA
2226	GCTGGGTCAATTGCTCGAGTAACCA
2227	TGGAGCGTTCTGGCAATGACCGAC
2228	CAAGTCAATTCTTGGCCAATT CGG
2229	CGTTCATGCAAGGATCCCAGGTTA
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2231	CCTAACTCTCCCTTGAGGCCGTTTC
2232	ATCTCGCGAAGGTTCAAACATT
2233	GCGACAGATTACGCTGC GGTTTC
2234	AAGCCCAAGACGGCCAACACGTTAC
2235	TCAAGTTCAAATCACATCCCGTGG
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2237	ACCGAACTATGTTCCGGCATGGCA
2238	CGTCATCGGGTGTGCAATGCCGTT

	2239	CGGACGGAGTCACGTTGTGCACT
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	2242	GGAGCGGCCGAATGGTGCTCTTA
	2243	ACTAAGCAAGGCTTGGATGTGCGT
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	2245	GCGAGGCGAATTATCCGCGGATT
	2246	CATACGACACACCTTGGGTGCTA
	2247	TGCTTGGCTTAAACCCCCTT
	2248	CCGGTTGGAAAACGCAAATATCGG
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	2250	GTTGTTCCACCAGTGATCACGCAG
	2251	GCCGCTGACAAGATGATCATCGTT
	2252	CTTCATAAAGCCAACCGATGCC
	2253	CTGACTGCATCTCGAAAGCAGGGTG
	2254	ATTTCTTGGAGAATCGGCCACGT
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	2256	CCGATCCCGCACATCCGTATCCTG
	2257	TATCACCGGGAGCGTCTTATCGTG
	2258	TAGGGCTCGTGCACCGATTAGAGG
	2259	GCGTGGCACTCGCTTGTCTAGGTA
	2260	CTCAACGAACCTCAAGGGCCCTAC
	2261	AGCCTGGTATCGACCAATCCTGCA
	2262	TACCGCTTAGTTGGCCGGATCC
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	2264	GGGACCCCTAGCAACGTCACCTTA
	2265	CTGCCTCCCCAGGAGTCATTGGAT
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	2271	CCTCCTGATTGGGAGTGCCTGGATT
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	2275	GGTGACCATGTGGCGTTTAGCTT
	2276	CACGGTTGCGCACGGTACCGAAC
	2277	CCTTATTGTTGGCTCCCTGCC
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	2280	CCGTCGGTGGTAGGACGTGAATGT

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	2285	CCACCCCAACTCCAATCTTCTCA
	2286	GTGCAGTAGACGGACTACCGCGTC
	2287	TTCGCCCATCGTATCAAGCAATT
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	2289	CCAGCACTGCCATCGGTTATAAT
	2290	CGAACCGTAGAACCTCGGTCGGTG
	2291	GCACCATGACAGAGCCCCAGGATG
	2292	TGGGCTACCGCAGAATAAGGGTGA
	2293	TGGCCTGTCGTGTCGAAGGAAACA
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	2300	CGCGATGGTTCTTAGCAAGACGAT
	2301	TACACCAAGGAAGAAATGGGGACG
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	2303	GTCGTTGTCGGCATTAAACGGC
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	2305	CGGACACTGTTTACCAAGAACCA
	2306	TACCCATGATGCGGAAGAACGTA
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	2308	CGGGAGATGAGAACGGTTTGTC
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	2310	AAAAACAGTTCGCGCGACTGTCGT
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	2312	TGGCTAGGGATGGGAATCATCTT
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	2315	TCCCTACGCGCATGACTCGCTTAC
	2316	TGGTCGATCACCTGTGACAGACGC
	2317	TGGGGTAGTCGATGCAATTG
	2318	CCCTGCCAGGATTACTATTCCGGA
	2319	TCCCGCACGGGAATTAAAGTAGA
40	2320	GTGATGTGCAGGAACCTCTGTCGC
	2321	ATTTAGGCATGCATGCGCTTCTCA
	2322	TTCGGCGCTAGTGGACGCCGTCAA

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	2323	GAGCTTCATCTCATCAGTCCGCG
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	2326	GGTCCCGAATTGTCAACCCTTC
5	2327	GCGCTGGATAGTCTGCCACCATGAA
	2328	TGAGTCCAGTGCTGCCACCATGAA
	2329	TTGAATTGGGTGTCGGAGCGTTCT
	2330	CGGCAGGGCAGACAATGCTTGAAC
	2331	GGGTCTGTCAAAGAGGGTGTCTGG
10	2332	CTTGTGCAAGACGAAGCACCCCTT
	2333	ATCGAATTCCGAGGGAGGTCTCCAT
	2334	TCCGACCCCTCAGAGTCGACTCATT
	2335	ATCAACGGCCACCTCCTGCCGAG
	2336	AGCCACGGAATAATTCCGTCCACC
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	2338	TCCACGCCCTTACCATCAACTGCAA
	2339	GCCAAGCGATAGGCCAGAACTCAG
	2340	AGCGTGTGGGTCAATTAGCACGA
	2341	GTTATGCGCGGCTTACGAGTCGA
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	2343	TCGGCAGCCAATGATCATAACCTCT
	2344	TAAGCCCAGTCGGTCTGTGTTT
	2345	ACATGGCAGACTAACAGGCCTCGC
	2346	CATGGCTGCACTCTAAGTCGAACG
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	2348	CTCGTGTCTCCAGAGGATTGTCCC
	2349	TGAAGGCATCAACCCAGAGGATT
	2350	ACAGCTCGAAGGCAGCCACATTGG
	2351	ACAACGAGTACCGCGACAGAAGGG
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	2353	ACAACTCAGCACTTCGACGTCCA
	2354	CGGGTTACTGGGTATCACCAATGC
	2355	CATCGGTTATCGCTGCACGCGCGT
	2356	GAAGGAATCCCGGATAGTCCGTGG
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	2358	AGCCTGCGACGTTCCCGACAGAC
	2359	AAGAAAGGCGCACGGGATCGATAT
	2360	TGTCGCGAAGCCAACTTCAAGTAA
	2361	GCGGCATGCAAGGTAGGTCTGGAT
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	2363	GCGTGCATAAGTTGCACATTGTGC
	2364	TTGAGGTAGCGTTTCGCCATAT

	2365	ATCCCACTTGTGAGAGGGCGCATT
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	2367	GCGTATCTCGGGTCGAACACTTG
	2368	ATGCCATTGAACTCGCACTTGCG
	2369	CGATTCCCACATATAATGTGGTCC
10	2370	CAATTTGGATAATCCAGCCACGCC
	2371	CGGCTTACCCATGATTCCGTGCA
	2372	GGTGGACCATGCCTGTGGTATGA
	2373	TATTTGTCGAAGATCGCAAGCGCC
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	2375	AGGGGGTGGGAAATCTGACAAAA
	2376	TGCTTGCTATCCGAAAAAGCAGG
	2377	TTATCGGATCAAATTGGCTTCGG
	2378	TGCAGCAACGAGTTACCCGGACTT
20	2379	TATACATGTCCGGAGGGGACCCA
	2380	TGCAAAACCGGAGGGATGAACCCTT
	2381	TCGGTCTAATGTCCACGCAGACAC
	2382	ATGTGTTGCCACCGCTCCTATT
	2383	TGGCGAGGCACGGCTTAATTGG
25	2384	GCGACGACCCGAGCGACTTTACA
	2385	CTCAGAGAGTCTATCCGGCGCCCT
	2386	GGAACATCTCTGGTCCCTCAGA
	2387	GCAACGCAGGGAAGTACTTAGCGA
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	2391	CGTGAGCCGTGGGTGTCTCTGTA
	2392	TACCTTGGTCGTCTCCGCTTTGT
	2393	TCGCCGAAAATGCTACGTGAAAA
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	2395	AAAGGAACCTGGCCAACCTATGG
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	2400	CCACACGGGCACGGAGTAATATCT
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	2414	GGCCTTCGGCATTAGACGGGTTG
	2415	CGTGATAGGCCACAGCGCTCAATT
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	2417	CGGGTATGGTTGATAAACAGCGTGG
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	2429	ACGGCTTCCCTAGTGTCCAGCCCTT
	2430	CTGTCAGGTCTACCCATGGCTC
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	2439	TGACCTGAAGCCCATCCATAAGCA
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	2444	TGT CCTGACAATCAAGGTGCAGG
	2445	AAATTGCACTCGCGGAGATTTCCT
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	2460	AATCGAATTCCCAGCGGCTGTT
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	2648	TGAGGACCATCCAATGGATCGGTT
	2649	TCGGTGTGGTAAATTGGATCCG
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	2652	CGGTACAGCGGATAGCCAAGGATA
	2653	CCATGCTTCGCTGCAGCATACT
	2654	CGCGGCAAAGATTAATTCCGGCG
	2655	GAAGACCCGTCCGGGTTCCATAC
40	2656	CTGGCAAGGAGGATGTGGCTCGTG
	2657	CTGTGCAGGGGTGGCTCTGTTGA
	2658	TTCAATAATGATCACGAGGGCCCA

	2659	TGGTGATGCGAAGCCTTACCTTG
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	2661	TTTGCCCAGCTCTCGCAGAACGTTA
	2662	AATTCAAGACGCCACATCGACGGTC
	2663	CCGTGGTCTGCCTCGATTACCTAC
	2664	GGCGAGGAATTCGGAACCTTATG
	2665	ATCCGATGATCAGATAACCGGCTGG
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	2667	TGTGGACCTAGAAAATTGCCAGCC
	2668	GAATAATCATCGCGTCCTCATGG
	2669	GGGATTGGCTTGGTGGAAAGAA
	2670	ATTGTGCTTCCTCGAACTGGGAAA
	2671	TGCCCCACCCCGTAAGTCAATAAT
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	2673	CCAGCCGTCACAGTGAATTCCG
	2674	CTTAAAGAGGCGCGAAGCACACA
	2675	TACCGCTCGTCGCGATCACATGA
	2676	CCGAGTGCAGCGAAGTGTATGTG
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	2678	TGCAGGCTTCTCAACGGCTGGAG
	2679	CTCCGTACGTATCCCGCGTGATAC
	2680	GGAAGTGCAACTTAAAGCCCCGCC
	2681	CGAACCGGCAGTCGATCGTTGCAT
	2682	CCGTTAGTGGTCGACAGTCGGTT
25	2683	TCAGGGCTACGCCCTCAGCACTACA
	2684	TATACGGGCCGAGGTCCGTATTG
	2685	CCAACGTGTGACGAAGGGCCATTG
	2686	CTGCTCAGCGGTGCTGAAAGACA
	2687	GGAGATTGACTTCGCGTTTACCA
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	2689	GAGTGGAGCATTCTCGGCCCTCAA
	2690	TGGATTGAAACCAATCCGCACAA
	2691	TGCTCTGTGGTCACTCGAGAGGA
	2692	TTGGGAGCACGGTTACCGCCTGTG
35	2693	CAACGCGAGCTAACGGTAGTTCG
	2694	AACGCTGAGCGCTCACCTCACCT
	2695	CCGTCGTAGATCTGGAGGCTCAA
	2696	GGATGGCATGGGCACACTGTAACC
	2697	TCGCTCGTAGATATCCTCACGCC
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	2699	CGGTGTGCTCAAATGCCAAAGGA
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2701	CGGCGGTACTTTCCACTGTCTT
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2704	CTCGGGCCTGTACAGCAAAGCCGT
2705	TGCGCGCTAGTGCTGCCTATGATC
2706	CCATCCTTGCCTTGAGGTAAGG
2707	AACAACAGCGTAAGACGGACAGGG
2708	GAGGCGGTCGAGGCTCACAAATT
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2710	AACTTGCTATAACCGGGCGCAGCAA
2711	CGCGGTGAATCGCATACACAGCGC
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2727	GGCTGCTCAGTGACGTGTCAACTG
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2731	AGCTACGTGTCCTCGAGCAAAAGCG
2732	TCAGGGCGAGTTTTTCAGCGGCG
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2739	TGAGGTGCGTCCCTAAGTAATG
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	2743	GGCTGGATTGACAATTAGCCCC
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	2745	CGCATCTGCCCAATTGTCCCTT
	2746	GTCGGCCTAGTCGGCAGAACGGTG
	2747	TCGACACCGTAGCAGCGTGGACA
	2748	TCCCTCACCTTCAAAAATGTGCT
	2749	GGGCAAGAACATGAGAACAGACCG
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	2751	TGGCGGTTGCATGTGATGATCAAG
	2752	CCTCGCGTGAGTAAAACCGTCCG
	2753	ACTTCCGCCACAGAACATGCCGCCAG
	2754	GTGTAGAGCTGGTAGCCCCGTT
	2755	CGCAGCATCCGAGTTAACACACAT
	2756	ATGAGCCTGGGATGATCCGCTGGT
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	2758	GCGCATGAAAAACTACGACGGACG
	2759	AAAGATGGGTCGATGGGAGCGTCT
	2760	ATCCTGGGCACGAGCGGATTATC
	2761	TCACCGCATTGATAGTTACCGCA
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	2763	CACAATGAAAAAACAAATGGCCCCA
	2764	CCTTGGCGCGCTTGTGGTACCAAC
	2765	CCGAGACCTTGGCACACGAAAGA
	2766	ACCGCGGTGTACACCTGAGCAGGC
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	2768	TCGTAATTGACCGACACACGCAG
	2769	CCTAGACGGATAACCTGAGCGGAA
	2770	AAGCGACAGCAGAGGTTAGTCGC
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	2773	TACCCCTCCGGACCAGCTGTAATGA
	2774	TATCCGCACGGTATAGCAGTTGCA
	2775	CATCAGTCGGCTACCTTCAGCCT
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	2778	CCACTACGGATCAGCACAGGTGTC
	2779	GGCCGAGACCACCAAGTAACAGGTT
	2780	CGCGCGGAAGCATTGAAGTTACTA
	2781	TCGGCTTACCGCTTCGTCTGACTT
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	2783	AGAGGAAGGAGGGCTGTGACAGA
	2784	TTCCAATGCGAGAGATGGCAGGCT

	2785	AAATGGGGTGCCTCGAATATGTGG
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	2787	CCGACTTTGTTATGTTGCTGGCG
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	2789	TGAGCTGGCGTCAACTCCGAAGA
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	2791	CGACAGCAATCCACATGCATTCTT
	2792	TGAATGGTCGGGAAACCAATGCAT
	2793	CTTGATCGAGATGCGGGTAGC
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	2795	CCACTACGCCATCCTGACAACGAG
	2796	TAGTAAGGCCAATGTAAGCCGTCC
	2797	GTCATGCATATGGGGCTGTTTC
	2798	ACCGGTAGACGTTAGCGGGTTCAA
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	2800	GACACAAACTGCAAGGGAGGCATG
	2801	CTCGAGCGCTGTCATCATATCGGC
	2802	GCGGCTAAGGCACAAGTAGACGTG
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	2804	GCCAAATGTTGGAATTGCTTCG
	2805	CCGATGATGTAAGCCGTGGCCCT
	2806	AGGAGCAAACAAACGCCAGTGACA
	2807	ACGAATTGGGTAGCCGGACTGAGA
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	2809	AGACAAGTCAGGAACGCCGTTCCG
	2810	AGACGACGCCAGATACGCTGCCA
	2811	AGGAAGCGCTTCTCCGGTTCTTC
	2812	GATGGACGCAAACACAAGGCATGC
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	2816	GTAAAGGAACCCCTCGGGAAATCCT
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	2819	TTCTCAGGCTGGCAAGAGTCGT
	2820	CGGACCTGGGATGCTGGATTAC
	2821	TCGAGCCGATAGGGTTGGCATTGC
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	2823	TGTGAAATTGCGTTTCGCATCTT
	2824	TTGCAATGCTCCAAAAAAACTGCC
	2825	TCTCATCATGGCTGTGGCTTGAC
	2826	ATTACACCGCTTGGTTGGAGTGG

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	2828	GAGATCAGACCGTGTGGATGCTG
	2829	CCACCTATCTTGATGCGACCTGGA
	2830	CCGATCGCCGTTATGTCTACGGC
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	2832	GATTCTCGCTTCCCAACGAGCATA
	2833	CCAGAGCAGCATTCCACAATGGTG
	2834	TGTGAAATGTGGCAGTCTCAGGGA
	2835	CGATCCTGCGTGCCTCATCCAGGC
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	2837	TCGCCTCCGCCCTCGTGTGAGAAG
	2838	TTCGCTTCAGCTCATTGAAACGA
	2839	TGTAATCTGAACAAGCGGACCCCT
	2840	TGGAATCTTCTTGAGCGCCGTGA
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	2842	TGATCCGAGCCATTCCAATCACC
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	2844	AGGCATCGGTAAGAAGGCCCTATG
	2845	CGCCGCGAGACCGATCCTTATTATT
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	2847	ACAGAAAGGTGGGGAGCCTAGCGT
	2848	AGGCTTGCACATGGGTAGTGAC
	2849	GCGTGGGCCTTGCTCCTGTTAAC
	2850	GAATACAGAGCGTCCGATGTGCC
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	2852	GGTGCACTCATGCGTCCGATCG
	2853	CTGTCCCACGGGAAACCTTACTT
	2854	TGGCTTACTGTCGCAATCTAGGCC
	2855	GCACTCAGTTCCGGTATCCATG
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	2857	GTAACGCCCTTGCCCCAGCGTAT
	2858	GCATTGATATGGTCGGTCTCGCCT
	2859	GTGGGTTAACGTGACAACGGACGC
	2860	CAAAACCCCTGCCGAAGATGTTGGT
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	2862	CGGGGAAGAACGGATTGCTAAAT
	2863	TGGTTAGCTTATGTCGGAGCCACC
	2864	ACGCGTCGATGAACTAAGGCTCGC
	2865	TTCTCCTGACGAGTACGCAGTGGG
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	2867	TGGCGCATTTCAAGGGATGATG
	2868	TCTTTGGTCCTGGTGTACGCG

	2869	GAGAACTCCCGCTACAAAGGAGCC
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	2872	CAACAAACCGCCTTGGGAAAGTGAC
	2873	TTGAAGGCCACCGATACTGATCGC
	2874	TCGTAATAGAACTGCGCCCAATGC
	2875	GGCACGTTGCCCAAGTTGGATCCA
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	2877	CTTGGCCGCTTGCAGTGCTAAA
	2878	AGTTCCCGCGTCCACTTCAACGCT
	2879	AATGGCTGCCAGATACCGCAGCC
	2880	CAAAAGGCCTGTCCGAACTTTCA
	2881	CGTCCACTTAGGTGGAGATACGCC
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	2883	AACATCAAGCGGCAATCTCCCTTC
	2884	CGTCCTGACATTATTAGCGCGTGC
	2885	TGTGCAGACCTAAACGACCTACGG
	2886	TTAGGTGGCCTAGACCCCTCGTA
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	2888	AGACCTTCCCACCGCGAGATGCTAC
	2889	TTCTTGCCAAAATGTGTCCAACCA
	2890	CAGTTTCATTGCAGCGAAAGCAA
	2891	GTGCCGATCCCGAGACAAGTTCCG
	2892	CATCCGGCCTCAGTGATTCTTACC
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	2894	GAACGGCCAGGGGACAACATATCGT
	2895	TCATCTAGGTGCAAGCGCAAGACA
	2896	TTTGGTTACCAAGCACCCATGTTCC
	2897	GACAACAGTCTGTCGCCACATCC
30	2898	GCCAACAGGAGATGCTTGACCAT
	2899	CTAAGGACGCATTGACCCCTGAAC
	2900	GGTCGCGTAGTGAGTCAGAGCGT
	2901	TTACCTCATGAACCCCTCGCGGCG
	2902	TATACAGCATCGTCGCCGGGCATA
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	2904	TGCACTCCGCAACCTTGTGAAATC
	2905	AACCCGTCATGCCGACTCCATCTA
	2906	AGCACTAGTGGCGTGCAGACTTGC
	2907	TAAAAAGTGCCGCTAACACGGAG
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	2909	TTCTGCTATGCGTATGGGGCCCG
	2910	CGAACTACTGCGTCAGCCTCTCCC

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	2916	ATGACTTCAGGCACCTCAGCACCT
	2917	CGGACGTGACAAACGGACATAACCC
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	2919	GAACCCTTATCGGGATAGGCCAA
	2920	CAGGACGATACCAAGCAGAACGCC
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	2922	AAACAACCATCAATGTCGGGTCCA
	2923	TGTAAAGACCAGTTGGCGGCTCTC
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	2933	CGTCGATATGTCGGCTATTGCCT
	2934	AAATGCAGGGTTAACAGAGGAGGCC
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	2937	CCCTCGATGGTCATTGGGAAGAC
	2938	CCTGTTCGCTCATATGGTGGGGT
	2939	GAAAGAACGATCGCGGAATAGCTG
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	2941	TCCTCCGTGAACCGCTGTAGCGCA
	2942	GCCCCAGAGAGTCCCTGCTCCCTA
	2943	TTGAGATTTTACGGTTCCCCGC
	2944	CGATAGGACGTGGGCATGTCCCAG
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	2946	TCACCGAGCTAGAGTCGCGTTACC
	2947	AGATAACGCCACTGACGACATGC
	2948	ACGCTTAGAGCTCCGATGCCGAAT
	2949	GGGCGATAACTAAATTGTGCCGC
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	2951	CGGCTGGTAGAACTGTGCATCGTA
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	2957	GTGACGGTTGATTAACGACCGTGG
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	2964	ACTTGCCGGACGACAGCAAAGAC
	2965	CACCGCGGTAGATGTATCCCTTCC
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40	2992	TAAATAGGCGAAACCGTTCGTGGC
	2993	TCAAGACCCGCAATGTGTTCATGT
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	2995	CAGGCGTAAACCTGAACCAAACGG
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	2998	CCCTGCACGATTAAAGCCACCTGTA
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	3025	AGGTTGGTAGGAAATGGAGCGCT
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	3028	TTTTCCGCCGCAATGTGATCTAA
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	3032	CCCTATATCGAGCCCATAAGGGCGA
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	3053	ACTCCGCTTCAATGGAGACCGTTG
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	3074	GATTTGGCGTCTCATTGCGTGAT
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	3076	GAGGTGCCATGTTAGTGGTGTCC
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	3082	AATAACACGGCGGTAAACAGACGA
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	3086	ACGAACAGGTAGGGATCGGTCTC
	3087	TGGATCCACCTTACCGCGCCATCG
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	3089	GAATTACATTGTGGATGGAGGCAGG
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	3092	AAATGACATCCGTTGGCCACAGC
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	3097	TACCCGAGAATTGGAGAACAGCG
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	3099	CACAGTGTCCAGCCCTTGACGAT
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	3101	TGGCATATTAAGATTGGCGACG
	3102	ACTGAAAAAGAACGGTAGCGGG
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	3105	CTGCCAGATCATTGCGCGATCCG
	3106	CGGAGGTTAAATGCTTAACCGGC
	3107	AGGCGTCTCAAACGTCTTCTGT
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	3116	AGGGATGCAGAGGCACCATGTT
	3117	CGGTCGACGTATGAGCATCCGCA
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	3120	CGAAGGGTTGTGCAATTACCGA

	3121	AAAACGCACCGCAATGACAAAATT
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	3123	CCTACCTGCCTGCTAGCGGTGAGG
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	3127	GGCACCCAATACCACGAAGAAGAA
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	3131	CCCCAGGGCGTAATGCACCATAG
	3132	GCAGGTCGAACGCTAGTGGTGAA
	3133	GGAACTTAGGAGGTCACGTCGCCA
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	3136	GTTTTGCAGCGCATGAGGTTCTTA
	3137	TTGCAGCTGATGCCAGCAGTACTA
	3138	GATATCAGGCTTCCCCTGCGC
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	3143	CGTAGCCTCCACCGTGTGATAG
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	3147	GTCCTGGACAGACGGAGGGTGTAA
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	3152	CATACCTCCCGCTTGGATTCACTG
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	3154	CACGGGACATTCAATTACAGGACG
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	3157	TCATGACAGCGCACCCATACCAT
	3158	GGTAGGGACTATCGATCGTGTG
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	3165	GGCATGGCTATGCCTCACACTAG
	3166	GGGTCTGTATTTCAGCATCGTCGT
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	3168	CTGGATTGGTACGTCCAACGTTT
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	3174	AGCTCTCTCGAAGTAGGGCGGTA
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	3180	TGCGTATTGATGCTCACAGCTG
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	3190	TGGCACTTGTAGTGCTGCGGTGG
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	3212	GGTCGTCCGACGTAAAAGACCAA
	3213	GTTTCGAGCTCTTCTCCGCAGG
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	3222	TTGATCACTGGATTGGGTGCGAAC
	3223	TCTGCAGACGTTGCGAGAGATGAT
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	3227	CTCGCTGGGTTGCTGGAGTAGCAC
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	3242	TGCCATCTGACCTGGTATTGCGT
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	3246	GGAGCGCCAGTATAATGAACGTG

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	3263	GCTTGTGGAATCCGACGGTTCCA
	3264	CACATCCACCCCTACTGAGGCACAA
	3265	GCCGGATGAATCTGCCTCGCTACA
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	3269	AGGGTTGTCGAAACATGGGGTGA
	3270	ACGCGACCTGCTGTCAGCGTGGTG
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	3274	GGCGTCCACATGTAATTGGGTCT
	3275	CGCATCACGATCGTTAGGAGGGAG
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	3277	TTTCCATAATTGACACCAACCGCG
	3278	GACCATGAGATGCTTTCTGCGC
	3279	CGCGGTCGTCCCTAGAGAATGTTG
	3280	TGCTGTGACGATGGCTCCTACCCG
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	3282	AAATGCACAGCGGAACGACGACACA
	3283	TATCACCTGGAACACGATCGGTT
	3284	CATTGAAGTCATGAAGCCTGGTGG
	3285	CTTCAACCGTAGTGGCTTGGCA
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	3288	TGAAATTGTGAGGGAGCCTAGCG

	3289	AGCGGGATCCCAGAGTTCGAAAA
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	3292	GTATT CCTGACCCGCTGAGTGTG
	3293	GCAGCGTATGGGGTAGCCAATGA
	3294	CGCCCTGGTGGAGTTGTATGATGA
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	3298	ATT CATGCAGGAAGTCCGAGGGAA
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	3306	GCAACGAGAGCGAACGGTTA A C
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	3313	CTCGGGTTCTGAAAGCGATGCTTC
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	3324	CCAATACCTGGTGACC ACTCCAA
	3325	GACGTCTGTTATGTCGTGCAAGG
	3326	CCACAACGTCGAAATGACCTACCA
	3327	CTTGGTGGCATGCATGCCTTGC
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3331	CGTCCCCGCGAGTTCATGGTGCTA
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3369	ACTTCAGCTCCAGTAGCACGCA
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	3503	TGATTCTCGATGTCACGCCGAACA
	3504	GATGGTTGCCCTTGTCGCAGC
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	3507	GACCAAGTGCAGGCGTCAGTCTGG
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	3518	AGCGTACCATCGATGGGATTCGA
	3519	TGGCCTCGCGATCACCACGATGTT
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	3521	CGTTAGTAACGATCGTCGGTGCAA
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	3532	TCTCAGTTAACCGGTGATCGGG
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	3576	CAGGTGCCATCGAGCGCTT TAGTG
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3605	TGTAAGTTGCCA ACTTTGCGGGTT
3606	GCACACCACCGGCAGATATCAAGA
3607	GTGTGGTTGTGAATGCGTGGTGA
3608	CAGCTGC GGCCCCACCTTCGATAC
3609	CAGCGAAGGACGACTACTGTGCAC
3610	CAGCAGTTCGTTGCTCCTGATTG
3611	AAACAATGGAGTGTACCTCCCGCA
3612	ACTATACGAGCATCATGAGCCGGC
3613	CTTGATAAGGTGGATTCCGGCA
3614	TTTAGTAGAACGCTGC GCGCGGTG
3615	AACTGAC GTTGAATAAAACCGCG
3616	GCTTTGTTCTACCGCGGATCATCA
3617	TGATATGCAGCGGCTCGGC TTAT
3618	CGGGAGTGC GTTATGTCCATGAT
3619	CAAATACCGGGAACGGATCGAAGC
3620	GATCAAGCCGAATGCTTGCAAAG
3621	AGAGAGGATGC GCTCCGGTTAGAG
3622	CTTAGTCAGCATA CCCGGGGCAG
3623	GTGTCTGGGGCGCAGGACCTGTA
3624	AACGCTCCACTGCCGTGATTCACT

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3625	GATCGTTGAGTCATCCCGTGGAGT
3626	CCTGGCCGGGTGCAATACTACAGT
3627	CGTAGCCCGAACGTAAGGGTCAGC
3628	CTGTGGCTTCAAGAGGATCCGTTG
3629	CTTGGGTCGGTGTAAATGTCCCTCGA
3630	GCCGTTGTGCCTATTCTTACGGA
3631	TCGCACGATGGCTAGAACGAGTAA
3632	ATTTGTTGCAATGGATGGCTCTG
3633	CGAATATCCGCTCGAACCTGACAA
3634	AAGTGGCGTGCGTCATAGCGCGAC
3635	TGATGTCCCTCCACACCGTGAACT
3636	CAAATGAAGTCGGGCCAATATTG
3637	GATGCATAGCGTGATTCCGGTGTG
3638	GTGACCGTAGAACGCTACCAGGGC
3639	ATAAGGACATATTGGCCTGGGGA
3640	AGATCTCACAAACCGAACCGGACG
3641	GTTGCGTTGGGGCGTCATAACAA
3642	TGTGAGGTITCTTAAGGCGAACG
3643	CATCTGGTTGCGAACGAACTCA
3644	TTCCCTGTCACAGATTGTCGGCCTT
3645	AACTTACCGATCCCTGAACGTGCA
3646	CCTATTCTGGACATGCGGCCACAT
3647	GTCGATGGGAGCTCCAGTTGCAT
3648	CGACCGTGAGGGTCCATACGTAGA
3649	TCTCGTTGCACGCACTGGGCCA
3650	ACTCCGCCAATGAAGGAATAGCT
3651	CCTCGACCTGGCGTGATGGAAGGC
3652	TAACAGCCGTTTGC GGTTACAA
3653	GCCTCCTGCAGTACGGTGTCTGTT
3654	GGCAGTCGGTCCCACCTAGTTGCA
3655	TAATCCACGGTTGGTGGAAAGTC
3656	CGGTGCAAGATCCTGGTTGTGTGA
3657	TTTCACCACTACCTTAGGTCGGCG
3658	CATCCCGTACCGGGAGGACAAGTC
3659	ACGAGGTAAAGGGATCCGTGCTGG
3660	CTAATAGTTGGCAGAGGGCGCT
3661	AGCATGGTAACCCCTGAGCCAGCAG
3662	GGAATCCTTGTGGGAACAGCCGAT
3663	CTGATGTGGAAAGAGGGTGGGAC
3664	ACTTTTGCAATCCGGCGTTGTA
3665	GCGATGACGTGACGAGTTCTCACC
3666	CCAGGTATTGAGCCCCGCCATATA

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	3667	TTGGACGTCCCTCCGAATATTGGCA
	3668	GGTAAGTGCAGGGAAAGTACGCTGAC
	3669	CCGCCTGAACCCTCGTAGGGATTA
	3670	CGTTTTGAGTAAGGATTGGCGA
5	3671	TGTGGTATTGAGGCATAGGTGGCA
	3672	TCCGGAAGGAAGGCAGCGATATGGC
	3673	GTTGAGCGAATCGGACGGCTTAC
	3674	TGAGTCTCCGAACGACAAGCGATC
	3675	AGTGAAGAGGGAGAGTCCAACCCG
10	3676	GTGAAGCCTGACGAATCCAACGTG
	3677	GTGCAGGGCTGTATCCCCATGACT
	3678	GTGGGTTTCCTACACACCGGATGA
	3679	GCGCCGTCGACTCTCTCAGCTGC
	3680	CTAGGCCTGCCATCACTGAGCAAT
15	3681	TTGGTGATGACTCATGCCAGACC
	3682	TATCTCCCGCGGGGTATATTACCG
	3683	CCGAGGGACACGTATCCCTGTTCG
	3684	TATCCCAGCACGCATTGATCT
	3685	TGATGATAGAGCAGGGTGCCGTCA
20	3686	GTAAGGAGCACACATTGGATTGG
	3687	CCCTTACTACGCCAGCCCTTTG
	3688	GTACCAGGGGGTGTGCTCCAAGGG
	3689	TGACCAGGCGGACCAGACGGTTT
	3690	CGTAAGCGGCGGTAGGTGTGCTAC
25	3691	CGCGGGGAGGGATCAGCAGTTTG
	3692	AAAGCGTATCCAGAAAGGCCATGG
	3693	AAGAAGAGACGCATGCTGGACGT
	3694	TGGCCATTGCGGGAGGTGGCTTA
	3695	AACGCCGAATTGAGGAGGCCGTTA
30	3696	GCCTCATTACGACATTGGCAGCAT
	3697	TCGAACCGCATTTGAAATGCC
	3698	AGGAATTCTAGCCGAAAGCCCTGC
	3699	TCCGCTGGTGGTGCTCTGGTTG
	3700	GTCGCGCTCCGTCCGATAGTATGA
35	3701	TGTGCAAGGACGGATGATTGACT
	3702	GGACAAGCGGCAACCTGGAGAAG
	3703	ATGCGGTGGCTACGGACTAATCCA
	3704	TGCACCGAGGTGGAAAGCAGGCTT
	3705	AGATTGTGGAGTTGTACGCTCC
40	3706	AACAGCAGTGAGGGCTGAAGCTG
	3707	CTGCCTGTTCCCTCACGCTCCAT
	3708	CCAATCCACTTGAGTCACATTGCG

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3709	CATTCTACCGCCCAACTTTGCAA
3710	CGGAGAACCATGCTGAGCAGTCCA
3711	GACTGTTCTCCAGAAAGGGCGAT
3712	AAATAATTGCTCACCGGAAGCGC
3713	GGGCCTGGAAGACCAACCAAATAC
3714	ACGACCGAGCACGTAGATATCAA
3715	TACGGGATCCTCGTGGCTACATCT
3716	CAAAGTCTCCCCGACCGAGTTGAC
3717	CCCGAGGCGAAGATCTCTAGGCAC
3718	AAAATTCTGCCACGAGACCCCTA
3719	CTGTGCGCATTCAAACACATCAC
3720	CATGGAAATGCCAGCTGCCTCCAT
3721	CGCGAAACCACAGTCCTCGTCGGG
3722	GTCCGCAGCTGTCCCAGACATTGGT
3723	GTCTCATTGGGACGATCGTCTCGA
3724	AGAGCGTTGCATGCTTGGCTCGG
3725	CTTCCGCCCCCTGTTGCAATGAGG
3726	TTGCGGTTCATACCGAAGCCAACA
3727	TGCGCGAGAATCGTCGTACGACG
3728	TGTATACCGTAGGGCGTCCGTGGGG
3729	TGCGGGGTATAGGGCTTCCTTATG
3730	ATCCCAGCCCAAGCAGCAGACGCA
3731	GTTCTGGCCACAGGAATGGCGT
3732	CACATGGGCATTAATTGCTACGGC
3733	ATAAGTCGGTCTGCCTGGCAATGA
3734	ACCTCGAGGCTGAGAACGTCAAAA
3735	GCGGAACGCTAGCCCCTTATGGTT
3736	TGCGAGGCTCTGGAGCAATCCAA
3737	ACAGAAGGGCGATCGCTCTGGCTG
3738	GGTTGGCAAGGGGCCAGCTCCTAC
3739	ATCGCTTCGCTCATGGAGTCCGA
3740	CGTCCCGATAGGCCGCTTGATCT
3741	GAATTCTGAGGCCGGCATTGTCCAC
3742	CAGCCCCATCAGTATCGGCTCGTA
3743	TGGAGAGTCGGATCCGTAGCGTCA
3744	TGGATCCAGTGCAGTCTGGCCG
3745	ATGCGGTGCGCTTGGAAATCCTCT
3746	ATCGCACTGCCCGTCAAAACAGC
3747	CACGTCTCCGCCCGAACACAAC
3748	AAGACAGTGGGTGAACGCACGGTA
3749	ACGCGCATAGGTGGTCAAACATCG
3750	CCCGGCGGTAGAAAATTGACAACCT

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3751	AAGGGATACTCAGGCGCCTGTTT
3752	CTTCTCTTGTGCAGGGCTCCCGT
3753	TTGAAGGGACCTGCCAAATGGCGA
3754	ACGCATGACGACGTCCAGTACGGG
3755	AAATGGATGTTACGCCGGCAAGCT
3756	TCGTGCGAGGCCTTCGGCATAAC
3757	TACATCGCGTCGAGTCATTCTGG
3758	TCACACCACATAATGGCACACGT
3759	CAGGTTACGGTTGAGGAGTGCAG
3760	GGTGTACACCGCTTCGTTGTCCT
3761	ACAATAATAAGGGAGCATGGCCG
3762	TCGGGTCCCTATGATCCAGTCCAA
3763	ACCCATTCCCTCTCGGGCAGATCAA
3764	TCGCAGGTGTAGACGGACGAAAAG
3765	CTCTTGCCTAGTAATCGGCCGCA
3766	TTCCGTGTCACCGCAGCCTGCTT
3767	ACTCTAAGTAGGGCTGGGTCGCGA
3768	TTGGTGGCTGTAAAGGTGCTTGGC
3769	CCGAATTACCCATTACACGGCAC
3770	GATGGATAGGTTCGCTTCCCACAA
3771	ATGACGGAAAGAACATGTGATTGGC
3772	ACGGTTCGGCTCTGTTAGTCACG
3773	GGATCCCGTAATTGAGGCGGCCAC
3774	ACCCGTTAACGTCGACGCCCTGCAGG
3775	TTCGATGTGAACGGTTGGCCAACC
3776	TCGATCGGAGTCTACCGCCATGT
3777	AGCAACGAGTTATGAGCGCAGGA
3778	TGGGAAACGAATGGGTGGCGGTTG
3779	TCTGTGTTGCCACCTACAGCAA
3780	CCTGCATTGGATGTACCCGCCGGT
3781	GAACGAGGTCCGGGTTGCATCTC
3782	GGCGCCGAAGCAGAACGACCATAT
3783	AGGCATCACGCATCAGGTACTGG
3784	TTTACAAAAGCATGGCCCTGGGA
3785	CCCAGGCAGGTCAACCAATTGTAGA
3786	CTGCAGCACGTGCCTGAAATTGCGT
3787	CCGTTTGCTCCAGCTATGAGCGT
3788	ATTTGTGCCGCATTGGGGTTATTG
3789	TAAGCAGAAAGCCGCAACTCCGGT
3790	GCGACTGATATAGTGCCTGGACCG
3791	AACTCTATTCTGACACCGCCCCGAA
3792	GTGCCTCCAAGAAGAAACACACC

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3793	ACGACCAGCGGCTGAGATCTAGG
3794	ATCCCCTCCTCAGGTGACGCTGT
3795	TGACATA CGCGTACCCAGCACAG
3796	TAACCGCGACTCTGACTCCCTGT
3797	AAGCGGTTGATCTGTGCAATCGG
3798	CTGTCAACTCGGTGTCGCCACAG
3799	AACTTGCCGTTAGGGCAGGTGA
3800	GCTGAAGAACCTCCAATTGCTGG
3801	AAGATGCGATGGTCAGTCCTCGT
3802	ACCCACCTCTGAAGGTTGAGACGG
3803	AGGCTACGCACCCCTCGAGAGTGAC
3804	CGGTACGAACGTGGTCCAGTTT
3805	CAAAGCAACGCGCGCCACTAAAAA
3806	ACGAGGAAGGAACTGATCCCCAGT
3807	TTCGCCACTATGGGCTCAGCATTA
3808	CGCTCGGCAGAGGAGTCCACTCAC
3809	TGTTGGCACGACTCCGTCCATGAA
3810	TGCCTACCCGGTGATTGCGACATC
3811	CAACGGTCGGATCTGAGGAGATCT
3812	CGTTACGAAGCGAAGTTCCCGAGT
3813	AGTGACGGCAAAGTCGCCATTCT
3814	ATT CAGCTGGGCATAGGCATGGG
3815	TAGGACAGCGTGGCTGGTACACA
3816	AATTTGTCCAGCTCTGCACGACCG
3817	TGAGTGGCTGTGATCCGTTCCAC
3818	TGTGGTGACACGCCAGAGCTGGTT
3819	CCTCACAGGTGTGAGAGGAGCCGC
3820	AGTCCCGCTTCTGCAAATCCGAA
3821	TCTGCGCCTACCCGTAAAGCTGAAC
3822	GCCTCCTGAGTTGATT CATGCATG
3823	CCTAACGGTTGGTCGCCGTTTT
3824	TCGCAAACCCACGAATGAGTCCCG
3825	AGTGCTAAGGTGGCGAGCAGAGG
3826	CTGGAGACTGCCATGGCAGGGTTG
3827	AAGGGATAGT GATGGCGATGGACG
3828	CTATCCACGGTGATGTCCGCCATT
3829	CGGACTAGAACCTGCCAACGACGA
3830	AGAGCCGGATGGCATTGCATGAAC
3831	AGTTGGCTAGCGGTGCAATGAGCA
3832	GCATGCGGTACCGCTTCAATCTAA
3833	GTGAGATTCCAAGCTCGCCGGTGA
3834	GCCATCCACCGCACAAATGAACGCT

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3835	GGGTGGTCCCACTGTGGTGGCA
3836	AGGC GGCTACGACGAGCGTCGTTA
3837	GCCAAGTGATCGTGCCTCCGCGTA
3838	TAGCCGTTATTCCCTTGATGCCG
3839	ACTATGTGGGACGAGCGCTGCGA
3840	GCACCTTCGAGAACCCATCAGATG
3841	ATTTTCTGTACCGATGCTCACCGG
3842	CACTGGAGCAATAAATGCCAGGC
3843	GGGTTCACGTATCTCATGGATGCG
3844	GCACGCTCCCAGTATGCTCCCTCA
3845	GAAGGGACTTAGTCCGCGGCCCTC
3846	TTCGTTACCCATAAGGGCGTTGCA
3847	GTTCCAGGTACCGACGAGCTGCGC
3848	TCGTACGTAGTCACACCGCGACTT
3849	GGGCTGGAGTAGCGGTCTGCTATG
3850	TAGCGGCACTCGTGTGCGAGTGG
3851	ACGTTGGGTTCTGACACGGCGATT
3852	TGTTGCTCGCCCCAAGTGATCTT
3853	CCCAGGTGTTACGGTGCATCACA
3854	CCTAGTGCACAGGCAAATCGGGCT
3855	GGCGTTCTCCAAGATAAGGCCAA
3856	ACTTCGATAACCGTGGACCTCGCCA
3857	CTGAGCGCGCTAACGTCCCTAGC
3858	ATCAGATAAACGATCCGACCGC
3859	CATGGCTGAATTGTCGACCCCTCT
3860	CGAAAGCGAGCAAATAGAATCCCC
3861	AGATTGCCCTGCGGCAGGTTGAAT
3862	AAGAGGC GGCGATCAGTTAGAAA
3863	CTGATGCCTGTAAGGAGGCGCTCG
3864	AATCGCGAGGTTGGCAGACAAAG
3865	CGTTGGGACACGGACC GTTCACTC
3866	AGATGTGTGCACTCGCGGTCACTT
3867	CAACTCGAGTGGCGGTAAACATCTG
3868	ACCAAGGTTGCGATTACGGGAAGC
3869	CGAAGCGGTAGACGGCTCGCGTTA
3870	TCTCGCGAACAGGAGGGAAGGCGT
3871	GTCCC GATTGCGCTGTGAGGAAA
3872	TACCACCGCGTGGCACGGAAATGG
3873	AAATGCTACCCGATTGCGCGGGAT
3874	TCGATT CAGGTTGTGCTGCGGAG
3875	CCATCTCATCCCACTATGGCATGC
3876	CTGGCCCGTGTGGTTGAGTCGA

	3877	GACACACACGTTGCAGGGCTCCC
5	3878	TCGAATCGAGTCGATCGTGAAGGT
0	3879	GAAAGCACTCGATCGCGTTGGATT
5	3880	AATTACCGCAACATGGGGCGTCAA
0	3881	GTGCTAACACTGTGGTCGTTCCA
5	3882	GGTAAGCGCCAGCCAGGAGTTGTC
0	3883	GGCGATCGTTCAGGAATCGCGTCA
5	3884	CTGGCTAGACCTCCGACACAGGCT
0	3885	CGGGTTAACGCCAACTGGCCTAG
5	3886	ATCGCAGCCTGGCCGCCTAGTTT
0	3887	GGCGTAGCCTAGCAAATTATGCCA
5	3888	ATGACGCGACGGAGACAATACGGC
0	3889	GTTGCATCACGAAAATGCCGTCTT
5	3890	GAGTCATGCCTTCCTCGCTTACC
0	3891	TCTGAACCGGTTATCCCCAACCTC
5	3892	TGCCTCTGGTAGGCGCCCAGTTAC
0	3893	CTGACGGTTTCATTGGCGTGCC
5	3894	TGAACACGAGCAACACTCCAACGC
0	3895	CGGCGCGCGAAAGACTTGAACCTG
5	3896	GCTACGAGTACCCGTCGGAAACGC
0	3897	ATACCCAACAGCATGGAGCGACCA
5	3898	ATCGCATCGCATCGTATTACGGG
0	3899	CGGCCTAGAGGTGCGAAAGCTATC
5	3900	TAACGCTTTCCGAGGCCGATTCT
0	3901	TCTGTCTAGCACGCCGACCTGCT
5	3902	CTCATCGTTAGTCGGTCGTCGA
0	3903	TCGTCGAGCAGATAGCGGGTAGG
5	3904	TCGACCCACAGTCAGGACACTACCG
0	3905	TGCGATTCTATGATGTCCGAACGC
5	3906	CAAATGCAATGGCAAGCACTCACC
0	3907	TCTAATCCATCGTTTTGGCGA
5	3908	TCTCAACTCCGGTACGACGAAACA
0	3909	CTGAAGAGGGTAGCCTGGGAGCGG
5	3910	GGCACAAATTAAACGCGCCCGTT
0	3911	CAAAGGAGGGTCAAAGGCCAGAAA
5	3912	TTTGGCCCGTGACGAGAAAAAT
0	3913	AGGAATGTGCGTGGCACCTGTGA
5	3914	TCGTGATGACTGCCCTCCGAATCA
0	3915	CACGTCGACATGTTGGTACCTCG
5	3916	TTGCGGTAGTTGGTTACCAACCGT
0	3917	GCAGTGGCGACAAATACAGCTGAG
5	3918	ACGGCATGATGGAGGGATAAACGT

	3919	TGGGATAATCCGCAAGGCCATAGC
	3920	CCTAGCTCTGCTGCGTCTTCGCGC
	3921	TCCTGGAACTGCTGAAGGCAGCTT
	3922	CGAAGGCAGGATGGTAGTCTCC
	3923	AACATTGTTCCCATCCCAGAGCAC
0	3924	CCAGGCAAGAAACAACCACCGCCT
	3925	AAATCCACAGGCAGGCCAAAGCTG
	3926	GCTCACCGCAGACTCCGCGCGATA
	3927	TAGGTGGCGAGAGAGGCCACAA
	3928	GGCGTTGGTGTGTCGGGACCATGA
	3929	TCTGAATGCTTCCGTGCTTCGTG
	3930	ACGCTCTGGACCTCGCTCATTGA
	3931	TCCCTTATGCGCAGCGCTCGTGT
5	3932	TTGCCGTCCTGCAGCAGGTAGCTC
	3933	GGTCTAGTGGCAGCAAGGAGCGAT
	3934	GGTAACCGCACCAGCTTAGACACC
	3935	GTGGCGATTGGCTTCCTATGCATA
	3936	TCAAAATACGCCAGGAAGGGCAA
	3937	TGCCATGCAGTCAGGTACGATGGT
10	3938	ACAGGTTACGTCGTGTGTTCCGT
	3939	CTCATGACGAACGAGCGGTCTGCA
	3940	GTCGTGCGAGAGGCCAACCTTA
	3941	GCTGGCTGACGCTGTTGTAGAGG
	3942	GCTACAGTGCTGCGTCCCGTGCCT
25	3943	TTTACGAGCACCAAGCTGGCGTAG
	3944	ACGAGTTGACGGTCGTAGGGACCG
	3945	TCGGATGGTAGGAGGCAGATCGG
	3946	ATTATGCAGATCCTGTGCATCCGC
	3947	AGGGATGGAGACGAAGGAAGCATT
30	3948	ACCCCAAGGACCCGTATTCCCTAGC
	3949	GCACCATCCTGGGGCTTCTCAATG
	3950	TACAATCCGTGGACGTTGCTCAG
	3951	GGTAGGCGAATCCGACTGGCATAG
	3952	AGGACCGAACCCATGTGCAGCATC
35	3953	ATACACCGCACAGAACGACAGCTG
	3954	TCCCTGGCGGCCGTGTGTTATTG
	3955	CTCCACCGCGAAGGGCGCTTGTAAAC
	3956	TGGCCCTGCCATCCTCGGATTCAAG
	3957	TGTCTATTGCCAGCGTGTGAGCATC
40	3958	TGTTGTTGGCACGCCCTACGGCA
	3959	GTGCCTCAACCGTATCGTGGCGGT
	3960	TCCTCGAAGTAGCGTGACCGAAC

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3961	AAACAATTCCCTGCACTCTCGGCC
3962	CACAAACTCGTCGAGGCACACAGT
3963	GACGAAACGCTCGGCAGAAAGCCT
3964	TCAACTCACACGGGACAGCAGTTC
3965	TCACGTGGATGGGCTTAGCTGGC
3966	AGGTGTTGTTCCGACTGCCACA
3967	TCAACCCCTTATTCCCGAGCATTG
3968	ACCTCACACAAGCGTTCTCGTCGA
3969	AACAGCATGCGGTCGCTGGCTTC
3970	CACGGACACGTGTTACATCCGATG
3971	CTGGGAGCCTGCTGATACTGGTG
3972	CGTCCTATGGGCCATGGCCAGGAT
3973	GTCCCCAAATCTCGCTTACAGGC
3974	TCACAAACCTGTGCGTGCATTGTC
3975	CACACTCGTGGCTGCGTGGAA
3976	GCCTGCACTTACGGCTATCTGCC
3977	TTGGCGTGGCGATTACCTGTTATT
3978	TTTGCGGCTGAAGTTACAGGGTG
3979	CACTTAAGGGGCTGACCGAGCAAC
3980	AGAAAACGTCAATCCGCCACCTT
3981	AACAAAACGGCGCTCCAACAAACG
3982	GCCTCAATATCTGGTTGCCGCTG
3983	TTCCACAGTCAATGATGGCGTGC
3984	GATTCCCAGTCTACCCGCGAGCAT
3985	AGGCCAATTACGACCCCTGTCACGG
3986	CATGCGAACGTTCCGAGGAGACGG
3987	CACACGCGATGGGTTGTGTGACGC
3988	TCCGGTATTGCGCAGGAACCATAG
3989	AAGATTAGGTGTGCCGCCCTCAGG
3990	TCGTTACGCCCCACTCGACGATG
3991	ACTAAAATGCCAGGTTGCTCCCT
3992	AGGATGGCCACGCCGAATCAAAGT
3993	TGATGAAGCAGCTCATCGCTGGCG
3994	CCCCGATGGGTCTTGTGGACTC
3995	ACACGAGGGCTGCTGGTGAGGGCT
3996	TGGTCACCAATTGATGATCCGAG
3997	AAGGCCGCTTGCATGCGACAAATT
3998	CCAGTGTTCGTTCATGGTGGCGT
3999	CCGACCGCTACATAGGTGTGCGAA
4000	TGTTGAAGCCGTTCCCAGATGACA

TABLE 2

Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
1	TTCGCCGTGCGTAGGCTTTCAA	TTGAAAAGCTACACGACGGCGAA
2	TTCGAAGCGCACGTCCTTTCAA	TTGAAAAGGGACGTGCGCTTCGAA
3	AACCGGTGGGAATGGGACATCAA	TTGATGTCCCATTCCCCACGCGTT
4	CCGTCGCATACCGGCTACGATCAA	TTGATCGTAGCCGGTATGCGACGG
5	ATGGCCGTGCTGGGACAAGTCAA	TTGACTTGCCCCAGCACGGCCAT
6	TTGCAACGGGCTGGTCAACGTCAA	TTGACGTTGACCAGCCCCTGCAA
7	CGCATAGGTTGCCGATTCGTCAA	TTGACGAAATCGGCAACCTATGCG
10	CCGTTGCGGTGTCCTGCTCAA	TTGAGCAAGGACGACCGCAAACGG
8	TTCGCTTCGTTGGCTGCACCTCAA	TTGAAGTGCAGCCACGAAAGCGAA
9	GTCCAACGCGCAACTCCGATTCAA	TTGAATCGGAGTTGCGCGTTGGAC
11	TTGCCGCACCGTCCGTATCTCAA	TTGAGATGACGGACGGTGCAGGCAA
12	CATCGTCCCTTCGATGGGATCAA	TTGATCCCATCGAAAGGGACGATG
13	GCACGGGAGCTGACGACGTGCAA	TTGACACGTCGTCAGCTCCGTGC
14	AGACGCACCGAACAGGCTGCAA	TTGACAGCTGTTGCGGTGCGTCT
15	CGTGTAGGGTCCCGTGTGCAA	TTGACAGCACGGGACCCCTACACG
16	CATCGTCAAGTACCGCACTCAA	TTGAGTGCAGGTTACTGCAGCGATG
17	GGCTGGTTGGCCCCGAAAGCTAG	CTAAGCTTCGGGCCAACAGGCC
20	GTTCCCAGTGAAGCTGCGATCTGG	CCAGATCGCAGCTTCACTGGGAAAC
18	TACTGGCATGGAATCCCTTACGC	GCGTAAGGGATTCCATGCCAAGTA
19	ACTAGCATATTCAAGGGCACCGC	GCCGGTGCCTGAAATATGCTAGT
20	GAACGGTCAATGAACCCGCTGTGA	TCACAGCGGTTCTTGAACCGTTTC
21	GCGGCCTGGTCAATATGAATCG	CGATTCATATTGAACCAAGGCCGC
25	GATCGTTAGAGGGACCTTGCCTGA	TCGGGCAAGGTCCCTTAACGATC
22	TGGACCTAGTCCGGCAGTGAAGAA	TTCGTCACTGCCGGACTAGGTCCA
23	ATAAAACTACCCAGGACGGCGGAA	TTCCGCCCTCCTGGTAGTTAT
24	CATCGGTTCGCGCCAATCCAGATA	TATCTGGATTGGCGCAACCGATG
25	GTCGGGCATAGAGCCGACCACCT	AGGGTGGTCGGCTCTATGCCGAC
26	CTTGGGTCAATGATTCAACGTGCTA	TAGCACGGTGAATCATGACCCAAG
27	TGCCTAACGTGCTAATCAGCAGCG	CGCTGCTGATTAGCACGTTAGGCA
28	CGCATGTTGGAGCATATGCCCTGA	TCAGGGCATATGCTCCAACATGCG
29	AGCCACTGCATCAGTGTGTTCAA	TTGAACAGCACTGATGCAGTGGCT
30	GGTTGTTTGAGGCGTCCCACACT	AGTGTGGACGCCCTAAAACAACC
31	TCGACCAAGAGCAAGGGCGGACCA	TGGTCCGCCCTGCTTGGTGA
32	GACATCGCTATTGCCATGGATCA	TGATCCATGCCAATAGCGATGTC
33	GAAATACGAAGTCTGCGGGAGTCG	CGACTCCCGCAGACTTCGTATTC
34	TGTCATGAATGATTGATCGCGCA	TCGCGCGATCAATCATTGACAGACA
35	ATATCGGGATTGCGTCCCGTGAA	TTCACCGGAAACGAATCCCGATAT
36		
37		

38	GCGAGCGTACCGAAGGGCTAGAA	TTCTAGGCCCTCGGTACGCTCGC
39	TTACCGGCAGCGGACTCCGAATT	AATTCGGAAGTCCGCTGCCGGTAA
40	GTAATCGAGAGCTGCGCGCCGTCT	AGACGGCGCGCAGCTCTCGATTAC
41	CCTGTTAGCGTAGGCGAGTCGATC	GATCGACTCGCCTACGCTAACAGG
42	TAGCGGACCGGCAGAATGAGTTCC	GGAACTCATTCTGCCGGTCCGCTA
43	GGTACATGCACTACGCGCACTCGG	CCGAGTGCACGTAGTGCATGTACC
44	AATTCACTCGGACTCCCGCGGT	TACCGCGGGAGTCCGAGATGAATT
45	GCCAAATCTGGATTGGCAGGAATG	CATTCCCTGCCAATCCAGATTGGC
46	TGCATTTTGGTTGAGGCACATCC	GGATGTGCCCTCACCGAAAATGCA
47	CCGCTCAATTACCATGCTTCGCT	AGCGAAGCATGGTGAATTGAGCGG
48	CTCGGAAAGGTGCAACTTGGTGT	ACACCAAAGTTGCACCTTCCGAG
49	AATTGACCAGCAGAACGTCCTT	ATGGGACGTTCTGCTGGTCGAATT
50	GCCAGAGTCTCAACCTCACGGGAT	ATCCCCTGAGGTTGAGACTCTGGC
51	CCAACAACGGAACGGAACCCGC	GCGGGTTCCCGTCCAGTTGGTGG
52	GAGAACTGATCGCTGAGGGGCATG	CATGCCCTCAGCGATCAGTTCTC
53	GGCACACTAGACTTGTGGCACCGA	TCGGTGCCACAAGTCTAGTGTGCC
54	TCACATCCAAATATGGTCCGCGAA	TTCCGCGGACCATATTGGATGTGA
55	GTCTGCCGGTGTGACCGCTTCATT	AATGAAGCGGTACACCCGGCAGAC
56	CATCGCAGAGCATAAACACCCCTCA	TGAGGGTGTATGCTCTGCGATG
57	GTGGGTATCTATGGCAGAGGCGGA	TCCGCCTCTGCCATAGATAACCAAC
58	ACGAGGTGCGCTGAGGTTCCATT	AATGGAACCTCAGCGGCACCTCGT
59	GGAATGAGTGGACCCAGGCACATT	AATGTGCCTGGGTCCACTCATTCC
60	TGTCAATATGCGTCCGTGTCGTCT	AGACGACACGGACGCATATTGACA
61	TGATGAGCCTCAGGGTACGAGGCA	TGCCTCGTACCCGTAGGCTCATCA
62	CACCGCGGTGTCCTACAGAAATGA	TCATTCTGTAGGAACACCGCGGTG
63	TTGTTGCCAATGGTGTCCGCTCGG	CCGAGCGGACACCAATTGGCAACAA
64	TTAACCTGCGTCTGCCCTTCCT	AGGAAAGGGCAGACCGCAGGTTAA
65	AGGCGCGTCCCTGCCTAGTGACG	CGTCACTAAGGCAGGAACGCGCCT
66	TAGGGCGATGGCACGAAGCTCAA	TTGAAGCTTGTGCCATGCCCTA
67	TGCATAGAGCCAAAGTCGGCGATG	CATGCCGACTTGGCTATGCA
68	TTGAGAGGCAGGTGGCCACACGGA	TCCGTGTGGCCACCTGCCCTCAA
69	TCCGCATTGTGAGAAAAACGAGC	GCTCGTTTTCTCACAATGCGGA
70	GGCGGTTCCGTAGCTATAGGTGC	GCACCTATAGCTACGGAAACCGGCC
71	GGTAAAATTCTGTAGCCACGGC	GCCCCTGGCTACGAAATTTCACC
72	CCGACGGAGGATGAAGACAATCAC	GTGATTGTCTTCATCCTCCGTGG
73	CCAGTTGCCAATTCGCCAAA	TTTGGCGAATTGGGCCAAACTGG
74	GGATCTATTAGGCCGTGCGCACAG	CTGTGCGCACGGCTAATAGATCC
75	CGGATGTCACCGTTGGACTTCA	TGAAAGTCCAAACGGTGACATCCG
76	ATCGCAAATCCTGCTCGTCCCTAA	TTAGGGACGAGCAGGATTGCGAT
77	CAGGGCATGCAATAATCGAGGTTC	GAACCTCGATTATTGCATGCCCTG
78	CATGCGTTGATATATGGGCCAAG	CTTGGGCCATATCAACGCATG

79	CAGCTGCAGCTTGTGACCAACCAC	GTGGTTGGTCACAAGCTGCAGCTG
80	TTGTATGCTGCCGACCGGCAGCC	GGTCGCCGGTCGGCAGACATAAA
81	GATGGCGCCCGTTGATAGGTATGG	CCATACCTATCAACGGGCGCCATC
82	ATGAGAATGCCGGCAATCTGCTA	TAGCAGATTGCCGGGATTCTCAT
83	ATTGCACTGACCGCAGGCTCGTG	CACGAGCCTGCGGTAGTCAAAT
84	CAGGGAGAACGGTTAACGTTCCCGT	ACGGGAACCTAACCGTTCTCCCTG
85	AGGCCGGCGATCGAGGAGTTGGT	ACCAAACCTCTCGATGCCGGCCT
86	ACACGGTGGTCTCTGATAGCGACC	GGTCGCTATCAGAGACCACCGTGT
87	GTGCAACGCCGAGGACTTCCATCA	TGATGGAAGTCCTCGCGTTGCAC
88	TCGGTGCCTGATAGCCATTCCGAT	ATCGGAATGGCTATCAGGCACCGA
89	TGAAATACCAACACAGCCAATTGGC	GCCAATTGGCTGTGTGGTATTC
90	GCATCGTGTACATGACTGCCGCGA	TCGCGGCAGTCATGTACACGATGC
91	CAGTGTCTAACGGCGCGTGTGAA	TTCACGCGCGCCGTTAGAACACTG
92	CGCTTGCAACGTTGCACCTACTCT	AGAGTAGGTGCAACGTTGCAAGCG
93	CGAAAAACTAGTGGGCTGCCCGCG	CGCGGCGAGCCCACTAGTTTCG
94	CTTCAGGGGAACGCCGGAGTCG	CGACTCCGGCAGTCCCCTGAAAG
95	TTGTGGCCTTCTGTAAAGGCACG	CGTGCCTTACAAGAAGGCCACAA
96	TCCACGAACGGCGACCCGTTGTCT	AGACAACGGGTCGCCGTTGTGGA
97	CGACCTTGACGAAACCTAACGAG	CTCGTTAGGTTCTGTGCAAGGTG
98	GTGCAGCTTACGAGCCAGCCTGA	TCAGGCTGGCTCGTGAAGCTGCAC
99	CGCTTCGTGCGAATAGACGATGA	TCATCGTCTATTGCAACGAAAGCG
100	TGCGCTTACAGGCTCTAGTGGTC	GACCACTAGGAGCCTGTAAGCGCA
101	CACCGCGCTTAGTCGCGATCGCATA	TATGCGATCGCGACTAACGCGTG
102	CGGAGGGAGGGAGCTAGCCTTCGA	TCGAAGGCTAGCTCCCTCCCTCCG
103	GCATCCGGCTTGTGATGACGCC	AGGCGTCATCAACAGGCCGGATGC
104	AGGCCAATCGATCTTATTGCCGAG	CTCGGCAATAAGATCGATTGGCCT
105	CCTTCCAATGATTGACAGCCCCA	TGGCGTATGCAATCATTGGAAGG
106	AACACTTGATCAGGCGGGTGTCT	AGACGACCCGCGCTGATCAAGTGT
107	TGGAATCAAGGCCGTAAAGGACAG	CTGTCCTTACGGCCTGATTCCA
108	GCTCCCGTAACCTGTCCACCAGTG	CACTGGTGGACAGGTTACGGGAGC
109	AGTGGTGAATGGCCGCTACCTGA	TCAGGGTAGCGGCCATTCAACACT
110	TGTTGAAGCGAGCTAAACGGCCA	TGGCGTITAGCTCGCTTCAACA
111	CAGCGCTCCAGAATTGACAGCAAT	ATTGCTGTCAATTCTGGAGCGCTG
112	AAGGTGGTGCCATTGATGGCTA	TAGCCAAATGAATGGCACCACCTT
113	CGTTAAACCGCAATCCGTTGGCT	AGCCGAACGGATTGCCGGTTAACG
114	CACGAGATACCGCGTAAGGGTGG	CCACCCCTACGCCGGTATCTCGTG
115	CTACGGCAAACGTGTGGATGGGT	ACCCATTCCACACGTTGCCGTAG
116	GTAGGGCGATGACGGCGAACTAC	GTAGTTGCCCGTCATGCCCTAC
117	AATCGACCTCCGCACACATTGCA	TGCGAATGTGTGCCGGAGGTGATT
118	GAGTCAGCATGGCGGGAGATTG	GAATCTCCGCCGCCATGCTGACTC
119	AGATAAAGACGCTGGCAACACGGG	CCCGTGTGCCAGCGTCTTATCT

	120	GGTACCTCAACGCGAACCACTTGT	ACAAGTGGTCGCCTGAGGTACC
	121	AAGCGATGGCTACCCAAGAGCGAT	ATCGCTCTGGTAGCCATCGCTT
	122	AGAGCTTATGCAGAACCAAGGCC	GGCGCCTGGTCTGCATAAGCTCT
5	123	ATCGGTCTCACGCAGGGTTGGATA	TATCCAACCCCTGCAGGACCGAT
	124	TAGGTTGCCGCCAGAAGAAACAT	ATGTTCTCTGGCGGGCAACCTA
	125	CGGTGCTGTTGCAAAAGCCTGTAG	CTACAGGCTTTGCAACAGCACCG
	126	TGATGAAAGTTGCGGCAGGACAC	GTGTCTGCCGAAACTTCATCA
	127	GTTGAGTGCAGGATGCAGCGATAG	CTATCGCTGCATCCTGACTCAAC
10	128	AACATTGCGCGGTCCACCAGGGTT	AACCCCTGGTGACCGCGCAATGTT
	129	GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCC
	130	TCGAGCTGGTCCCCGTGAACGTGT	ACACGTTCACGGGGACCAGCTCGA
	131	GTCTGGGGGCCGCTTAGTAAAAA	TTTCACTAAGCGGCCCAAGAC
	132	ACTGTTGGCTTGCTCATGTCCA	TGGACATGAGAGCAAGCCAACAGT
	133	AGGACCATTCGGAAGGCGAAGATA	TATCTCGCCTTCCGAATGGTCT
15	134	CTTGGGAGGCATCCGCTATAAGGA	TCCTTATAGCGGATGCCCTCCAAG
	135	AATAAACGGAACGCACCGCTACAG	CTGTAGCGGTGCGTCCGTTATT
	136	TTGTACGTGCAGTCCCCATAAGCA	TGCTTATGGGACCCACGTACAA
	137	CGCACCAAACGTAGTTCCCAGAC	GTCTGGGAAACTCAGTTGGTGC
	138	ACCTGATCGTCCCCATTGGGAA	TTCCCAATAGGGAACGATCAGGT
20	139	GGAACAGAGGGCGAGGGACTGAGC	GCTCAGTCCCCCTGCCCTGTTC
	140	CCCTGCCTTGGCGTCTGGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
	141	ACTCTGACACGCCAACCTCGGAAG	CTTCCGGAGTTGGCGTGTAGT
	142	CTGACGGTTTCATTGGCGTGCC	GGCACGCCAACGAAACCGTCAG
	143	TGCGGTGGTCATTGGAGCTGCC	GGCCAGCTCCAATGAACCACCGCA
25	144	GCATGGCCAACTAGTGAUTCGCAA	TTGCGAGTCACTAGTTGGCATGC
	145	AGGCCGTAAAGCGAATCTCACCTG	CAGGTGAGATTGCTTACGGCCT
	146	CGAATATTATGCCGAGAACCGCG	CGCGGATTCTCGGCATAATATTG
	147	ACAGACGAGCTCCAAACCACATGA	TCATGTGGTTGGGAGCTCGTCTGT
	148	GGACGGTTGTGCTGGATTGCTG	CAGACAATTCCAGCACAAACCGTCC
30	149	AAAGGCTATTGAGTTGGTTGGCG	CGCCCCAACCAACTCAATAGCCTT
	150	GATGGCCTATTGGAGATCGGCC	GGCCCGATCTCCGAATAGGCCATC
	151	GATCCAGTAGGCAGCTCATCCCA	TGGGATGAAGCTGCCACTGGATC
	152	AAATACTCGCGGGTATGCTTCT	AGAAGCATACCCGCGCAGTTATT
	153	GGAGGAGGTTGTCTCGAAAGCA	TGCTTCCGAGACAAACCTCCTCC
35	154	CTTGGTATGGCACATGCTGCCG	CGGGCAGCATGTGCCATACCAAAG
	155	AGAAAGGCTCGAGAACGGAACT	AGTTCCCGTTGCTCGAGCCTTCT
	156	AATCTACCGCACTGGCCGCAAGT	ACTTGCAGGACCAGTGCAGGTTAGATT
	157	CGTGGCGGCCACAGTTTGGAGG	CCTCCAAAACGTGGCCGCCACG
	158	TTGCAGTTCAATCCATACGCACGT	ACGTGCGTATGGATTGAACTGCAA
40	159	GGCCCAAAGCCCCAGACCAATTAA	TAAAATGGCTGGGGCTTGGGCC
	160	CGCCTGTCTTGTCTCCGGACAAT	ATTGTCCGGAGACAAAGACAGGCG

	161	TGAGGCACAGGGGCCAAAAACTA	TAGTTTTGGCCCTGTTGCCTCA
5	162	AGCGGAAGTAGTCCTCGGCTCGTC	GACGAGCCGAGGACTACTTCCGCT
	163	GGCCCCAAGGCTTAGAGATAGTGG	CCACTATCTCTAACGCTTGGGCC
	164	GCACGTGAAGTTAACCGCGATTC	GAATCGCGTTAAACTCACGTGC
	165	AGCGGCAGAACGTTCCGTACGG	CCGTCAAGGAACGTTCTGCCGCT
	166	TCGTCGAGCAGACGAGATTGACCG	CGTCAATCTCGTCTGCTGACGA
	167	TCTTGCCCGTAACTGACTGCTT	AAGCAGTCAGTTACGGCAAAGA
	168	TTTATGTGCCAAGGGTTACCGA	TCGGTTAACCCCTGGCACATAAA
10	169	TGTTACTGTGGTCACGGCAGTCC	GGACTGCCGTGAACCACAGTAACA
	170	CGCGCCTCGCTAGACCTTTATTG	CAATAAAGGTCTAGCGAGGCGCG
	171	ACAAATGCGTGAGAGCTCCCAACT	AGTTGGGAGCTCTACGCATTGT
	172	CGCGCAGATTATAGACCCGAATGT	ACATTGGGTCTATAATCTGCCGCG
	173	CAAATAACGCCGCTGAATCGCGT-	ACGCCGATTAGCGGGCTTATTG
15	174	CCTTCGTGCATCGGTGATGATGTT	AACATCATCACCGATGCACGAAGG
	175	TGAACACGAGCAACACTCCAACGC	CGTGGAGTGTGCTCGTGTCA
	176	CAGCAGATCCTCGTAGCGGTCGT	ACGACCGCTACGAAGGATCTGCTG
	177	GGAACCTGGTGAGTTGCGCTCAT	ATGAGGCACAACTCACCAGGTTCC
	178	TCATAAGCGACAATCGCGGGCTTA	TAAGCCCGCATTGTCGCTTATGA
20	179	CCCAACGTCACTGAAGCTCACAGT	ACTGTGAGCTTCAGTGACGTTGGG
	180	TGTCAGAGCCCGCAGACACGG	CCGTCAGTCGCGGGCTCTGACA
	181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
	182	CTCAGAAGTCCTCGCGAAGTGGG	CCCAGTTGCCGAGGACTCTGAG
	183	ATCCTTTATCTACTCCGCGGGCA	TCGCCGCGGAGTAGATAAAAGGAT
25	184	AGGCAGTCAGCAACAGGATAAAC	GGTTTATCCTGTTGCTGCACGCCT
	185	ACTCTCGAGGGAGTCTCTGGCACA	TGTGCCAGAGACTCCCTCGAGAGT
	186	TTGCCAGGTCCATCGAGACCTGTT	AACAGGTCTCGATGGACCTGGCAA
	187	TCCACTATAACTGCAGGTCCGTGT	ACACGGACCCGAGTTATAGTGGAA
	188	GCCCAGTCGGCTAAACCTTCTCGC	CGAAACTGTTAGAGCCGACTGGGC
30	189	CGGAACGGATAATCGCGTCAGGT	ACCTGACCCGATTATCCGTTCCG
	190	AAAATAAGCGCCTGGCGGGAGGA	TCCTCCCGCCAGGGCCTTATTTA
	191	GCGCACTCGTGAAACCTTCTCGC	GCGAGAAAGGTTTACGAGTGC
	192	AGTTTGCCAGGTACTGGCAAGTC	GCACCTGCCAGTACCTGGCAAAC
	193	ACAACGAGGGATGTCCAGCGGCAT	ATGCCGCTGGACATCCCTCGTTGT
35	194	TTCGCAGCACCGCTAGGTACAGT	ACTGTACCTAGCGGGTGTGCGAA
	195	TAACCCGATTTTGCAGCTCTGCC	GGCAGAGTCGCAAAATCGGGTTA
	196	CGTCGCATTGCAAGCGTAGGCTTG	CAAGCCTACGCTTGCATGCGACG
	197	GAGCTGACGTACCATCAGAGGAA	TTCCCTGTGGTACGTCAGCTC
	198	GGAGGCTGGGGTCGCGCTTAAGT	ACTTAAGCGCGACCCCCAGCCTCC
40	199	TTGTGGGAACCGCACTAGCTGGCT	AGCCAGCTAGTGCGGTTCCCACAA
	200	CCCTCGCACTGTGTTCACCTCTT	AAGAGGGTGAACACAGTGCAGGG
	201	TCATTGACTCGAATCCGCACAAACG	CGTTGTGCGGATTGAGTCATGA

	202	ACAGGGGTTGGCCTTCGTACGTAC	GTACGTACGAAGGCCAACCCCTGT
	203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGTGATGTTGCACGGCCT
5	204	GGGCCGTGGTCACGTAATATTGGC	GCCAATATTACGTGACCACGGCCC
	205	GCGCGGACATGAAACGACAAGGCC	GGCCTGTGTTCATGTCCGCGC
	206	CTTATTGGGTGCCGGTGTGGATT	AATCCGACACCGGCACCCAATAAG
	207	GGGGCGGTTACCAAAAAATCCGAT	ATCGGATTTTTGGTAACCGCCCC
	208	GCTAAAGCGTGCTCCGTAACTGCC	GGCAGTTACGGAGCACGCTTAGC
10	209	ATCTCATGCATCTCGGTTGTCGT	ACGACGAACCGAGATGCATGAGAT
	210	ACGAAAAAAGTGTGCGGATCCCC	AGGGGATCCGCACACTTTTCTG
	211	CCAAGTACACCGCACGCATGTTA	AAACATGCGTGCAGGTACTTGG
	212	ATCGTGCCTGGAGTGTGCGCATCTA	TAGATGCGACACTCCACGCACGAT
	213	TCCAGATACCGCCCCGAACTTGA	TCAAAGTTGGGGCGGTATCTGGA
	214	TCTGCTGGCAGCACGTGAAGTGGC	GCCACTTCACGTGCTGCCAGCAGA
	215	TTGAAATTGCTCTGCCGTAGTC	TGACTGACGGCAGAGCAATTCAA
15	216	AGTCAGGCGAGATGTTAGGCAGC	GCTGCCTGAACATCTGCCCTGACT
	217	ACAAGCCGACGTTAACGCCGCCA	TGGGCGGGCTAACGTCGGTTGT
	218	CCCTAATGAGGCCAGAACCTGCA	TGCAGGTTACTGGCCTCATTAGGG
	219	GTGAGACACACATCCCCCTCAATG	CATTGGAGGGATGTGTCTCAC
20	220	CGACGGATGCAGAGTTAGTGGTC	GACCACTGAACTCTGCATCCGTCG
	221	CCCGCATGCCCTGGCGGTATTACAA	TTGTAATACCGCCAGGCATGCGGG
	222	TTAGCAAAGCGGCCGCTTAGCAA	TTGCTAACGGGCCGCTTGCTAA
	223	CCCGACACGGGTCAAGCGTAATAAT	ATTATTACGCTGACCCGTGTCGGG
	224	GCGACGGCCCTGAGGTATGTCGT	GACGACATAACCTCAGGGCCGTCGC
	225	CAAAAGTGTGTTCCCTGCGCTTG	CAAGCGCAAGGGAACACACTTTG
25	226	TCTCGAACACAGCCGGTTATTG	CAATAACCGGGCTGTGCTTCGAGA
	227	ATGCTAACCGTTGGCCATGGAACT	AGTTCCATGGCCAACGGTTAGCAT
	228	CTTGCAGGTGTTAGCCCAGCGGT	ACCGCTGGGCTAACACTCCGCAAG
	229	TGCTCCCTAGGCCTCGGAGGAGT	ACTCCTCCGAGCGCCTAGGGAGCA
	230	CCAATGCCCTTGAGTAAGCGATGG	CCATCGCTTACTCAAAGGCATTGG
30	231	AGCAGATAACGTCCCAATGACGCC	GGCGTCATTGGGACGTTATCTGCT
	232	TTGACCATTACGTGTTGCGCCAT	ATGGGCGAACACGTAATGGTCAA
	233	TCGCGTATTGCGGAATTGTCGT	CAGACGAATTCCGCAAATCGCGA
	234	CTGCGTGTCAACAAATGTCGCCAG	CTGCGGGACATTGTTGACACGCAG
	235	TCTGGTGCCACGCAAGGTCCACAG	CTGTGGACCTTGCCTGGCACCAGA
35	236	CTCCGGGAGGTCACTTAATTGCGG	CCGCAATTAAAGTGCACCTCCGGAG
	237	TTTCGTGATTGCCGGAGGAGGC	GCCTCCTCCGGCAATCACGAAA
	238	TCGGGATGTAGCTGGGCTACCGG	CCGGTAGCCCCAGCTACATCCCGA
	239	CGAGCCAACGCAAACACGTCTTG	CAAGGACGTGTTGCCTGGCTCG
40	240	GCAAAGCCTTGTGGGCGGTAGT	ACTACCGCCCCACAAAGGCTTGC
	241	ATTGACCGGAAATGAGGTCTCG	CGAAGACCTCATTCCGGTCGAAT
	242	TTCGCTTGCTGAGTTGCTCTGTT	GAACAGAGCAACTCAGCAAGCGAA

	243	CGCGTGAAGACCCCATTCCCGAGT	ACTCGGGAAATGGGGTCTTCACCGCG
5	244	AACCGTATTGCGGGTCACTTGTGG	CCACAAGTGACCGCGAATACGGTT
	245	GGGGCCAACC GTT CGAGGCGTAT	ATACGCCCTCGAAACGGTGGCCCC
	246	TTCGGCTGGCAGTCAAACGGCTT	AAGCCGTTGGACTGCCAGCCGAA
	247	GGGTGTGGTTAGAATGCACGGTC	GAACCGTGCATTCTAACACACCC
	248	GCGAGGACCGA ACTAGACAAACGG	CCGTTTGTCTAGTCGGTCCTCGC
	249	ACGCACGCGTGACCGAAGTTGCTG	CAGCAACTCGGTACCGTGC GT
10	250	TAAAAGGTGCGTTGAAAGGGGGA	TCCCCCTTCAAAGCGACCTTTA
	251	TGCGATCGCTAACTGCTGGGACAA	TTGTCCCAGCAGTAGCGATCGCA
	252	GGAGGTATAAGCGGAGCGGCCTCA	TGAGGCCGCTCCGCTTACCTCC
	253	ATGCTGACATGTCGTGACCTCGT	ACGAGGTGCACGACATGTCAGCAT
	254	TGTGGTTAAAGCGTCCGTTAACG	CGTTGAACGGACGCTTAACCACA
	255	CGTTCACACCGGCGTAAGCTGCGT	ACGCAGCTTACGCCGGTGTGAACG
	256	CCTATCCCCGCGAGAACTTCTGTG	CACAGAAGTTCTGCCGGGATAGG
15	257	GTCTGCACTCACG CAGCGGAGGG	TCCCTCCGCTGCGTGAGTGCAGAC
	258	GCACGAGTTGGTGCTCGG CAGATT	AATCTGCCAGCACCACACTGTGC
	259	AACGTCG CACGACACACGTTGTC	GACGAACGTGTGTCGTGCGACGTT
	260	ATGCGCGCTTATCCTAGCATGGTC	GACCATGCTAGGATAAGCGCGCAT
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	262	TGTGCCTCATCCTTAGGATACGGC	GCCGTATCTTAAGGATGAGGCACA
	263	AGGTGGTGTGGGTCAACCGCTTTA	TAAAGCGGTTGACCCACACCA CCT
	264	CTGGATCGAAGGGACTGCAAGCTC	GAGCTTGCAGTCCCTCGATCCAG
	265	TAGATCAACTCGCGTACG C ATGGA	TCCATGCGTACCGCAGTTGATCTA
	266	GATCCTGCGGAGAAGAGAGTGCAG	CTGCACTCTTCTCCGCAGGATC
25	267	TACGTGTGGAGATGCCCGAACCG	CGGTTGGGGCATCTCCACACGTA
	268	GCGCTATGTCATCGTGGCGTAG	CTACGCCACGATTGACATAGCGC
	269	AGCGAGGTTCTAGCGTCGACACC	GGTGTGACGCTAGAAACCTCGCT
	270	ACCCAGGTTTGCCGTTGTGGAAT	ATTCCACAA CGGCAAAACCTGGGT
	271	CCCTGTTAACGGCTGCGTAGTCTC	GAGACTACCGCAGCCGTTAACAGGG
30	272	AGGCCGATTTCACCCGCCATTGC	GCAATTGGCGGGT GAAATCGGCCT
	273	GAGCCCTCACTCCTGCCCTTGA	TCAAAGGGCAAGGAGTGAGGGCTC
	274	GGGTGGACATCCGCCCGAGCTCA	TGACTGCGAGGCGGATGTCCACCC
	275	GATGGCTGAGAACCGTGCTACGGAT	ATCGTAGCACGGTTCTCAGCCATC
	276	TCGACGTTAGGAGTGCTGCCAGAA	TTCTGGCAGCACTCTAACGTCGA
35	277	CGAATGGGTCTGGACCTTGCATAG	CTATGCAAGGTCCAGACCCATTG
	278	GTGCACCA GACATTGAACTCGGA	TCCGAGTTGCAATGTCGGTGCAC
	279	AGAGGCCCGTATATCCCATCCAT	ATGGATGGGATATACGGGGCCTCT
	280	AACGCCTGTTCA GAGCATCAGCGG	CCGCTGATGCTCTGAAACAGGC TT
	281	AAGGCTCAACACGCC TATGTGCGC	GCGCACATAGGC GTGTTGAGCCTT
40	282	AGTCCGTGTTGCCAGATTGGCTCG	CGAGCCAATCTGGCAACACGGACT
	283	ATGTCCCATGTAAAGACGCGTGTG	CACACGCGTCTTACATGGGACAT

284	ATGGAGTCTGCTCACGCCAAAGG	CCTTTGGCGTGAGCAGACTCCAT
285	CGGCCTCCAACAAGGAGCACTAAC	GTTAGTGCTCCTTGTGGAGGCCG
286	CAGAGCCGTGGCAACATTGCGAGC	GCTCGCAATGTTGCCACGGCTCTG
287	TCATTTGAATGAGGTGCGCACCGG	CCGGTGCACCTCATTCAAATGA
288	GACGTACCGGAAGGCCGTATAAA	TTTATACGGCGCTTCCGGTACGTC
289	ATGCGAGCAATGGGATCCGGATTC	GAATCCGGATCCCATTGCTCGCAT
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291	CGCACCGTAAGTAGATTGCCCGC	GCGGGCAAATCTACTTACGGTGC
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293	TCCGCCTTTGGTACCTCGAAG	CTTCGAGGTAAACCAAAAGGCCGA
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295	CCGACAGCAGCCAAGACGTCCCAG	CTGGGACGTCTGGCTGCTGTCGG
296	CATAAAAAAAACCTGGGGCTCTGCG	CGCAGAGCCCCAGGTTTTATG
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298	GGCAGAAAGAGCGAAACCGGCTCGT	ACGAGCCGGTTCGCTTTGCC
299	GGGATGCGTATTTAGCGAACACG	CGTGTTCGCTAAAATACGCATCCC
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303	AACCTTGACCCGTGGATGACGCTA	TAGCGTCATCCACGGGTCAGGTT
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305	GCCTCTCTCGACGATGCGATT	AAAATCGCATCGTGAGAAGAGGC
306	GCTTCGGATGAACGGGATGGTG	CAACCATCCCCTCATCCGGAAAGC
307	CCCTCCATGTTCTGAACGGTT	AAACCGTTGAAGAACATGGAGGG
308	TTGATGGCGGCAATGCTCTGCT	AGCAAGAGCATTGCCGCCATCAA
309	ATTGTGAGATGCGCAAATTCCCC	GGGGAATTGGCGCATCTCACAAT
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311	ACTCCACTCTCGGTGGCAAAC	TAGTTGCCACCGAGGGAGTGGAGT
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315	AGACAGCGATCCGCGGCTCATGAT	ATCATGAGCCGGGATCGCTGTCT
316	CGCGTCTCTAACTGAGAGCAGCC	TGGCTGCTCTCAGTTAGAGACGCG
317	AGGCGCACATGTACGGACATTCA	CTGAATGTCGTACATGTGCGCCT
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319	TGATCCATATTGTCGGACGTTGCG	CGCAACGTCCGACAATATGGATCA
320	ACCTGCCGGGAGTTCATAGGCTAG	CTAGCCTATGAACTCCGGCAGGT
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322	GGTAATATTCAAGCGCGACCGCTA	TGAGCGGTGCGCTGAATATTACC
323	ATAGCGTACGACGAGGTGACGCGC	GCGCGTCACCTCGTGTACGCTAT
324	TAGGTACCGATGCGTTGACGCTA	TAGCGTAAACGCATCGTGACCTA

	325	ACTGCCCGTACCTCTGGTCTGGC	GCCAGAACCAAGAGGTACGGGCAGT
	326	CCTTGGCCTGAAGTTGTCGTAGC	GCTACGACAACCTCAGGCCAAAGG
5	327	GTGCCCGACGAGCGTATCGTTGA	TACAACGATAACGCTCGTGGGCAC
	328	AGGCGCTACGTGGGCCCTGGAGCAA	TTGCTCCAGGCCACGTAGCGCCT
	329	GGGTGCTACCATTGCATTAGTCG	CGGACTAATGCAATGGTAGCACCC
10	330	ACCACGCGCGTACGTGTAACCGAG	CTCGGTTACACGTACGCCGCTGGT
	331	CCATGATGCATTGGGTGCATTAG	CTAAATGCACCCAATGCATCATGG
	332	GGTCCGGCCCTACGAAACGTTGA	TCGAACGTTCGTAGGGCCGGACC
15	333	CCGTGTGGCTGGAGATTCGTGTGA	TCACACGAATCTCCAGGCCACACGG
	334	GTTAGGGCGACGCATATTGGCACA	TGTGCCAATATGCGTCGCCCTAAC
	335	GGGTCAGTCAGGTGCGTTAGGATC	GATCCTAACGCACCTGACTGACCC
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	337	GCCACCACCCAGTGCATTAGGTA	TACCTGAATGCACTGGGTGGTGGC
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	339	TGTTGCCGCCATTAGGGAGTAAC	GTTACTCCCTAATGGCGGCAAACA
	340	GCTCCGCTGGATGTGCCGGTTAG	CTAAACCGGCACATCCAGCGGGAGC
	341	CGGTAGCATGCGAGATCCCTGTTA	TAACAGGGATCTGCATGCTACCG
25	342	CTACGCTCTACCAGTTGCCCTGCGA	TCGCAGGCAACTGGTAGAGCGTAG
	343	GTGCCTCTGCTGTATTTGCCAAG	CTTGGCAAATACAGCAGGAGGCAC
	344	TTGCGACTCGACTTGGACGAGTAG	CTACTCGTCCAAGTCGAGTCGCAA
	345	TCTGGGAGCTGTTACTCCAGCCA	TGGCTGGAGTAAACAGCTCCAGA
	346	TGCACGCGGAACCTCCCTTACCAT	ATGGTAAAGGGAGTCCCGCGTGCA
30	347	TGGCAGCAAATGAATCGAAAGCAC	GTGTTTCGATTCTTGCTGCCA
	348	AACTGGTGACGCGGTACAGCGAAG	CTTCGCTGTACCGCGTCACCAGTT
	349	AGACGATTACGCTGGACGCCGTCG	CGACGGCGTCCAGCGTAATCGTCT
	350	ATGCCCTCCTCATGGAAAGGGTT	AACCCCTTCCATGAAGGAGGGCAT
	351	ATTCTCGGAGCGTATGCCAGAA	TTCTGGCGCATACTCGCTCGAGAAAT
	352	ATAGCGGAGTTGGGTACGCGAAC	GTTCGCGTACCCAAACTCCGCTAT
35	353	ACCTACGCATACCGCTTGGCGAGG	CCTCGCCAAGCGGTATGCGTAGGT
	354	GATTACCTGAATGGCAAGCGAGC	GCTCGCTTGGCCATTCAAGGTAATC
	355	CCTGTTAGCATCACGGCGCTTAGG	CCTAAGCGCCGTGATGCTAACAGG
	356	CGGAATGATGCGCTCGACAACGCT	AGCGTTGTCGAGCGCATCTCCG
	357	TGAGAGAGGCCTGGTTAAGGCAA	TTGCCTTAACCAACGCCCTCTCA
	358	AAGCAGGGCGAAGGGATACTCCTCG	CGAGGGAGTATCCCTCGCCTGCTT
40	359	TCACGACAGACGGGCCGAGATTAC	GTAATCTGGCCCGTCTGCGTGA
	360	AAGCAATTGGCCTCGTTGTGA	TCACAAAACGAGGCCAAATTGCTT
	361	GCTGGTTGCGGTAGGATCGCATAT	ATATGCGATCCTACCGCAACCAGC
	362	TTGTGAATCCGTTCTGCCCCGAC	GTCGGGGACAGAACGGATTACAA
	363	TGGGCTCCTCTGAGGCGAGATGGC	GCCATCTGCCCTCAGAGGAGCCA
	364	GGATAGAGTGAATCGACCGGCAAC	GTTGCCGGTCGATTCACTCTATCC
	365	TGCACCGAACGTGCACGAGTAATT	AATTACTCGTGCACGTTGGTGCA

	366	GCCAGTATTCTGGGTGTTGGACG	CGTCCAACACCCGAGAATACTGGC
5	367	TCGCTACCTAACGACGGGCCATAC	GTATGGCCCGGTCTTAGGTAGCGA
	368	TGGCATTGACGAGCAGCAGTCAGT	ACTGACTGCTGCTCGTCAATGCCA
	369	CGCGTCCCAGGCCCTGGAGTAT	ATACTCCAAGGGCGCTGGGACCGCG
	370	ATGAAGCCTACCAGGGGAGCTTCGT	ACGAAGTGCCTGGTAGGCTTCAT
	371	CCAGACAGATGGCCTGGAACCATG	CATGGTCCAGGCCATCTGTCTGG
	372	TGGCGTGGGACCATCTCAAAGCTA	TAGCTTGAGATGGTCCCACGCCA
10	373	CCGCATGGGAACACGTGTCAAGGT	ACCTTGACACGTGTTCCATGCGG
	374	GCCCCACTCGTCAGCTGGACGTAAT	ATTACGTCCAGCTGACGAGTGGG
	375	ATTACGGTCGTGATCCAGAAAGCG	CGCTTCTGGATCACGACCGTAAT
	376	TGCGAGGGTGGAGCACCTACGAGAGA	TCTCTCGTAGGTGCTCACCTCGCA
	377	GGGCCGCATTCTTGTGATGTCCATT	GAATGGACATCAAGAATGCCGCC
	378	CCTCGGATGTGGCTCTGCCTAG	CTAGGCAGAGGCCACATCCGAGG
15	379	TAGGCATGTTGGCGTGAGCGCTAT	ATAGCGCTCACGCCAACATGCCA
	380	CGATACGAACGAGGATGTCCGCCT	AGGCGGACATCCTCGTATCG
	381	TACGCCGGTTAGCACGGTGCCTA	TAGCGCACCGTGCTAACCGGCGTA
	382	CATACGATGTCCGGGCCGTGTCG	GCGACACGCCGGACATGTATG
	383	ATCCCGCAGTTGTATGGCGCGTTAT	ATAACGCCATACAACACTGCGGAT
20	384	GGGTAAGGGACAAAGATGGGATGG	CCATCCCATTTGTCCCTTACCC
	385	ATTGGAGTGTGTTGGTAATCCGC	GCGGATTACCAAAACACTCCAAT
	386	GAACCGAGCCAACGTATGGACACG	CGTGTCCATACGTTGGCTGGTC
	387	GCCGTCAAGCTTAAGGTTTGGG	GCCCAAAACCTTAAGCTTGACGGC
	388	ACCTGCTTTGGGTGGGTGATATG	CATATACCCACCCAAAAGCAGGT
25	389	AATCGTGGCGCAGCAAACGTATA	TATACGTTGCTGCCACGATT
	390	GTCGCCGGATTGCTCAGTATAAGC	GCTTATACTGAGCAATCCGGCGAC
	391	ACCCGTCGATGCTCCTCCTCAGA	TCTGAGGAGGAAGCATGACGGGT
	392	ATCCGGGTGGCGATAACAAGAGAT	ATCTCTGTATGCCACCCGGAT
	393	TTCCCGCATGAGTCAGCTTGAAAA	TTTCAAAGCTGACTCATGCGGAA
30	394	GCAAAGTCCCAGTGGCAAGCCGAT	ATCGGCTTGCAGTGGACTTGC
	395	CGACCTCGGCTTCATCGTACACAT	ATGTGTACGATGAAGCCGAGGTG
	396	CTCATGAGCGCAGTTGTGCGTGAG	CTCACGCACAACGTGCGCTATGAG
	397	CAGATGAAGGATCCACGGCCGGAG	CTCCGGCCGTGGATCCTCATCTG
	398	TCAAAGGCTTGGATACAGCCGT	ACGGCTGTATCCAAGAGCCTTGA
35	399	TCCGCTAATTCCAATCAGGGCTC	GAGCCCTGATTGAAATTAGCGGA
	400	ACGCACGGCGCTTGCCTTAATG	CATTAAGGAAAAGGCCGTGCGT
	401	TGACAACGTCACAAGGAGCAGGAC	GTCCTGCTCTTGTGACGTTGCA
	402	CTTAGTTGGGCGCGGTATCCAGA	TCTGGATACCGCCGGCCAACTAAG
	403	GCTCTAATGCCGTGGAGTCGGAAAC	GTTCCGACTCCACGGCATTAGAGC
40	404	CCGATTACAAATTGACTGACCGCA	TGCGGTAGTCATTTGTAATCGG
	405	AGACGTACGTGAGCCTCCGTGTC	GACACGGGAGGTCACGTACGTCT
	406	AATGGAGCGATACTGATCCAACGCA	TGCGTTGGATCGTATCGCTCCATT

	407	GGAGGCCTGTAAGCGCTA	TACGCCATCAGTACAGCGCCTCC
	408	TGTGGATTGACCAACACGGGA	TCCCGTGGTCATTCAAAACA
5	409	CATGTCTGGATGCGCTCAATGAAG	CTTCATTGAGCGCATCCAGACATG
	410	GCCCCGCTAACCGACACCCAGTT	AAACTGGGTGCGGATTAGCGGGC
	411	CCATTGACAGGAGAGCCATGAGCC	GGCTCATGGCTCTCCTGTCAATGG
	412	GAATCACCGAACATCACCAGTCGTT	AACGAGTCGGTATTGGTGATTTC
	413	AACCAGCCGAGTAGCTACGTG	CGACGTAAGCTACTGCGGCTGGTT
	414	TTTCTGAGGGACACGCCGGCGTT	AACGCCCGCGTGTCCCTCAGAAAA
10	415	GGTGCCTCCGTTGATCGATCCTCC	GGAGGATCGATAAACGGAGCACC
	416	CCGCTTAGGCCATACTCTGAGCCA	TGGCTCAGAGTATGGCTAACCGG
	417	TAAGACATACCGACGCCCTGCCT	AGGCAAGGGCGTCGGTATGTCTTA
	418	GTTCCCAGGCCAGTCATTGAGAC	GTCTCAATGACTGGCGTCGGGAAC
	419	TAAAAGTTCGCGGAGGTGGCT	AGCCCGACCTCCCGCAAACTTTA
15	420	CGGTCCAGACGAGCTGAGTCGGC	GCCGAACTCAGCTCGTCTGGACCG
	421	CGGCGTAGCGGCTACGGACTTAA	TTAAGTCCGTAGCCCTACGCCG
	422	GCTTGGATGCCCATGCGGCAAGGT	ACCTTGCCTGCATGGCATCCAAGC
	423	AGCGGGATCCCAGAGTTCGAAAA	TTTCGAAACTCTGGATCCCGCT
	424	GAGCTTGAGAGCGAGGTGATCCTC	GAGGATGACCTCGCTCTCAAGCTC
20	425	GCATCGGCCGTTGACCATATT	GAATATGGTCAAAACGGCGATGC
	426	CATAGCGCTGCACGTTGACCGC	GCGGTGAAACGTGCAGCGCTATG
	427	ACCCGACAACCAACCAATTAAAAA	TTTTGAATTGGTGGTTGCGGGT
	428	GCGAACACTCATAAGAGCGCCCTG	CAGGGCGCTCTTATGAGTGTTCGC
	429	CCGCCGAGTGTAGAGAGACTCCGA	TCGGAGTCTCTACACTCGGCCGG
25	430	GACATCGGGAGCCGAAACATGAG	CTCATGTTCCGGCTCCGATGTC
	431	TCGTGTAGACTCGCGACAGCGT	ACGCCTGTCGCCGAGTCTACACGA
	432	ATGCGCATATACTGACTGCGCAGG	CCTGCGCAGTCAGTATATGCGCAT
	433	ACAAGCGAACCGAGTTTGATGA	TCATCAAAACTCGGGTCGTTGT
	434	GCATGAGACTCCCGGAAGACATGT	ACATGTCTCGCGGAGTCTCATGC
30	435	TCCTACATGTCGCGTCACGATCAC	GTGATCGTACGCGACATGTAGGA
	436	GACCGATCGCGAACGTGTACACAT	ATGTGTACGACTTCGCGATCGGT
	437	GTCGCCAGGACTGGCCGATGTGA	TCACATCGGCCAGTCCTGGCGAC
	438	ACCGATAAGACTTGCATCCGAACG	CGTTGGATGCAAGTCTTATCGGT
	439	TCCATAACCAGTCCGAAGTGCCGG	CCGGCACTCGGACTGGTTATGGA
35	440	ACCGCCCTGCATCTGTATTTAA	TTAAATACGAGATGCAGGGCGGT
	441	AGACCGCATCAATTGGCGCGTACC	GGTACGCGCAATTGATGCGGTCT
	442	AGAGGCTTGGCAAGTAGGGACCT	AGGGTCCCTACTTGCCAAGCCTCT
	443	GCAATGGACGCCAGACGATACCGG	CCGGTATCGTCTGGCGTCCATTGC
	444	GCTGGACTTAGTCGTGTCGGCGG	CCGCCGAACACGACTAAGTCCAGC
40	445	AGGCATCGTGCCTGGATTGCTCCCT	AGGGAGCAATCCGGCACGATGCCT
	446	TGCGCATGTCGACGTTAACAAAG	CTTGTCAACGTCGACATGCGCA
	447	TTCGGGTACATCCGATGCCATAC	GTATGGCATGGATGTGACCCGAA

	448	ACCCATGCCGGAAAGCGATGTTG	CAACATGCCTTCCGGCGATGGGT
5	449	AAGCGCTGACTCGGCTAAGAACCA	TGATTCTTAGCCGAGTCAGCGCTT
	450	ACTTCCAAGTCCTTGACCGTCCGA	TCGGACGGTCAAGGACTTGGAAAGT
	451	TCTCAATATTCCCGTAGTCGCCA	TGGGCAGACTACGGGAATTGAGA
	452	AACAGTCCCTTTTCCCTGGCGC	GCGCCAGGAAAAAGAGGAACGTGTT
	453	CGTCCTCCATGTTGTCACGAACAG	CTGTTCGTGACAACATGGAGGACG
10	454	TGCGCAGACCTACCTGCTTTGCT	AGCAAAGACAGGTAGGTCTGCGCA
	455	ATGGACGGCTTCGCACTCCTCC	AAGGAGGACTGCGAAGCCGTCCAT
	456	TGAACGCTTCTATGGGCCACGTA	TACGTGGCCCATAAGAAAGCGTTCA
	457	TGAACCTGCGCGAGCGATAACC	GGTTATCGCTCGCGCAGGGTTCA
	458	GTTCTGCGCGATGAATCAGGACC	GGTCTGATTCATCGCGAAGAAC
	459	AGGGTACGTGTCGCAGCTCGCGT	ACGCGAAGCTGCGACACGTACCC
15	460	ACCCCTGCTCCGCCATGTCCTCA	TGAGAGACATGGCGAGCAAGGGT
	461	GGGACAAGGATTGAAGCTGGCGTC	GACGCCAGCTCAATCCTGTCCC
	462	TGTCGTTGCTCCGAGTACCAATTG	CAATGGTACTCGGGAGCAACGACA
	463	GTTGTCGAGACGTTGTGTCAGC	GCTGACACAAACGTCTCGGACAAC
	464	GCTGGTGAACACTCACGAACCGCT	AGCGGTTCGTGAGTGTACCGAC
	465	GCAGACAGGGCAAATCGGTGCAA	TTTGCACCGATTGCCCTGTCTGC
20	466	CCCCATCACAAACGAGTGGCGACTTT	AAAGTCGCCACTCGTTGTGATGGG
	467	GCTTCTACAGCTGGCGTAGCG	CGCTAGCACGCCAGCTGTAGAAC
	468	GAATGTGTGCCGACCAATTCTAGCC	GGCTAGAATGGTCGGCACACATT
	469	CCAGCGGAAGTTAGAGCTGTGG	CCACAGAGCTTAACCTCCGCTGG
	470	TTTTTACCGACCACTCCATGTGG	CCGACATGGAGTGGTCGGTAAAAA
	471	GGGGCTATGTGATGACGGCTAGC	GCTAGGCCGTACATCACAGCCGC
25	472	AGTACACGGCGTGTAGCGCTCC	GGAGCGCTAACACGCCGTGTACT
	473	TCCTGTGTTGGCGCACTCCAC	GTGGGAGTGCGCCACACAGGA
	474	CCAACTAACCAATCGCGGGATGA	TCATCCGCGCGATTGGTTAGTTGG
	475	AGTGAGTGACCAAGGCAGGAGCAA	TTGCTCTGCCCTGGTCACTCACT
	476	CATCTTCGCGGAGTTATTGCGG	CCGCAATAAAACTCCCGAAAGATG
30	477	CTTCGTCGGTTAGTGCACAGCA	TGCTGTCGCACTAACCGGACGAAG
	478	CTCACGAAAACGTGGGCCGAAAT	ATTCGGGCCACGTTCTGTGAG
	479	CGCAGCAGCTGAACTCTAGCATTG	CAATGCTAGAGTTAGCTGCTGCG
	480	AGGAGACATACGCCAAATGGTGC	GCACCATTTGGCGTATGTCTCCT
	481	ATTGAGAACTCGTGCGGGAGTTG	CAAACCTCCGCACGAGTTCTCAAT
35	482	CTCTTGTAGGCCAGGAGGAGCA	TGCTCCTCCTGGGCCTACAAAGAG
	483	GCCGCAGGGTCGATAATTGGCTA	TAGACCAATTATCGACCCCTGCGGC
	484	AAACGCCGCCCTGAGACTATTGGG	CCCAATAGTCTCAGGGCGGCGTT
	485	CTGAGTTGCCCTGGAACGTTGGACT	AGTCCACGTTCCAGGCAACTCAG
	486	CGGATGGGTTGCAGAGTATGGGAT	ATCCCATACTCTGCAACCCATCCG
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	488	GGAAATGAGAACCTACCCAGCG	CGCTGGGTAAGGTTCTCATTCC

	489	AACGCATCGTCCGTCAACTCATCA	TGATGAGTTGACGGACGATCGCTT
5	490	TGGAGAGAGACTTCGGCCATTGTT	AACAATGGCCGAAGTCTCTCTCCA
	491	TTGCGCTCATTGGATCTGTCAGG	CCTGACAAGATCCAATGAGCGCAA
	492	AGCGCGTAAAGCACGGCAACATT	AATGTTGCCGTGCTTAACCGCGCT
	493	AGCCAGTAAACTGTGGGCGGCTGT	ACAGCCGCCACAGTTACTGGCT
	494	CGACTGTGCAACCAGCAGCTG	CAGCTGCTGGTTGACATCAGTCG
	495	GGTTGCTCATACGACGAGCGAGTG	CACTCGCTCGTCGTATGAGCAACC
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	497	ACGCAGTTTATTCCCCCTGGCTTCT	AGAAGCCAGGGAAATAACTCGCT
	498	AGAACCTCCGCGCCTCCGTAGTAG	CTACTACGGAGGCAGCGGGAGGTTCT
	499	AAAGGAGCTTCGCCAACGTACC	GGTACGTTGGCGAAAGCTCCCTT
	500	AGTGATTGTGCCACTCCACAGCTC	GAGCTGTGGAGTGGACAATCACT
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	502	GGGAGACAGCCATTATGGTCCTCG	CGAGGACCATAATGGCTGTCTCCC
	503	GAGACGCTGTCACTCCGGCAGAAC	GTTCTCCGGAGTGACAGCGTCTC
	504	CCACCGGTCGCTTAAGATGCACTT	AAGTGCATCTAACGCGACCGGTGG
	505	CGGCATAACGTCCAGTCCTGGGAC	GTCCCAGGACTGGACGTTATGCCG
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	507	TGCACACTAGGTCCGTCGCTTGT	ATCAAGCGACGGACCTAGTGTGCA
	508	AGGGAACCGCGTTCAAACTCAGTT	AACTGAGTTAACCGGGTTCCCT
	509	GAATTACAACCACCCGCTCGTGT	AACACGAGCGGGTGGTTGTAATTC
	510	TTCAGTGCTCACGAAGCATGGATT	AATCCATGCTTCGTGAGCACTGAA
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	512	AATGCACCTCGACGAGCCTCATA	TATGAGGCTCGTCGAGGTCGCATT
	513	CCGAAACCGTTAACGTGGCGCACA	TGTGCGCACGTTAACGGTTCCG
	514	TAAAGTAACAAGGCACCTCCCGC	GGGGGAGGTCGCCTTGTACTTTA
	515	TAATGATTTAGTCGCGGGGTGGG	CCCACCCCGCGACTAAAATCATTA
	516	GGCTACTCTAACGTGCCGCTCAGG	CCTGAGCGGGCACTAGAGTAGCC
30	517	TGGCGGACGACTCAATATCTCACG	CGTGAGATATTGAGTCGTCCGCCA
	518	GGCGTCTAGGCATAATAGACCGTC	GACGGTCTATTACGCCAACGCC
	519	GCCACCTTAAAGCGCGCTCTAG	CTAGAGCCGCCGTCTAAAGGTGGC
	520	GAGATGTAAACGTGCAGGCACC	GGTGCCTGCACGTTACACATCTC
35	521	TAGCTCGTGGCCCTCCAAGCGTGT	ACACGCTTGGAGGGCCACGAGCTA
	522	GTGTCGGCGCTATTGGCCTTACC	GGTAAGGCCAAATAGCGCCGACAC
	523	CCAGGGAAGCAACTGGTGCATT	AATGGCAACCAGTTGCTCCCTGG
	524	TTCCGAAACTAACGCCAGAACCGCT	AGCGGTTCTGGCTTAGTTGGAA
	525	GCAAACCCGGTAACCCGAGAGTTC	GAACCTCGGGTTACCGGGTTGC
40	526	GCAAATGGCGTCATGCACGAACGT	ACGTTCGTGCATGACGCCATTG
	527	AGTACTTCGCGCCCAGTTAGGG	CCCTAAACTGGCGCGAAAGTACT
	528	AAGATCTGCGAGGCATCCGGCTT	AAGCCGGGATGCCTCGCAGATCTT
	529	GCAAGTGTATCGCACAGTGCATT	AATCGCACTGTGCGATACTTGC

	530	CCGACAAGGCCTCAATTCAATTCTG	CAGAATGAATTGAGGCCTGTCGG
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	532	ATCCAGAGATCCGTTTGAGCGT	ACGCTGAAAACGGATCTCTGGAT
	533	GTCACCAGGAGGGAAAGTTCACCC	GGGTGAAACTTCCCTCTGGTGAC
	534	TTCCGTCAGGCGGATCAACGGAAT	ATTCCGTTGATCCGCCTGACGGAA
	535	ATGCCGGACACGCATTACACAGGC	GCCTGTGTAATGCGTGCCGGCAT
	536	TGGGCCGCTTGGCGCTTCATAGA	TCTATGAAAGCGCCAAGCGGCCA
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	538	TTGGCCAGGAATATGGTCTCGAGA	TCTCGAGACCATAATTCCGGCCA
	539	GTCTCGGCCGACTTGCTATGCAT	ATGCATAGCAAGTCGGCCGCAGAC
	540	AACTTGCTCATTCTCAAGCCGACG	CGTCGGCTTGAGAATGAGCAAGTT
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	542	ACGGCCTGCGTCAGCACATGCATC	GATGCATGTGCTGACGCAGGCCGT
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	544	AGTCGCGGTCCCACGATTCACTT	AAAGTAATCGTGGGACCGCGAAGT
	545	TGCTCAATTGTGCAGAAAACGCC	GGCGTTTCTGCACAAATTGAGCA
	546	TTATCGCGAGAGACGACC GTGTC	GGACACGGTCGTCTCGCGATAA
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	549	CCAAATATAGCCGCGCGGAGACAT	ATGTCTCCGCGCGGTATATTGG
	550	GCAAACCTGATTGAATCGTGCC	GGGCACGATTCAATCAGGGTTGC
	551	TAGCGTCTGCGTAAACCATGGG	CCCATGGTTTACGCAAGACGCTA
	552	CCACCCCCGACAGCGCTGGACTCTT	AAAGAGTCCAGCGCTGTCGGGTGG
25	553	ACGAGCACTGAAGGCTGCTTACG	CGTAAAGCAGCCTTCAGTGCTCGT
	554	CATATCAGCGTCGTCTAGCTCGCG	CGCGAGCTAGACGACGCTGATATG
	555	TGATCCCGGACCGGCTAGACTAAT	ATTAGTCTAGCCGGTCCGGGATCA
	556	GGCCCCGACACTACAGGGTAATCA	TGATTACCTGTAGTGTGGGCC
	557	GGCTCCAGGGCGAGATTATGAATG	CATTCTAAATCTGCCCTGGAGCC
30	558	CAAATCCGATGGCGGAAAATTA	TAATTTCCGCCATCGGATTTG
	559	CACAGGCGCATAGGGAGCAAGCTA	TAGCTTGCTCCCTATGCGCCTGTG
	560	TAGCTATTGCCCGATGGGCTACT	AGTAGCCCATGGGGCAATAGCTA
	561	TGGTACGCGGTCCATAGCAAGTCG	CGACTTGCTATGGACCGCGTACCA
	562	GACGCTGTGGCTCGGAAACTGTTC	GAACAGTTCCGAGCCACAGCGTC
35	563	CCTGGGTTCGCCGCGTGGTAACG	CAGTTACACGCGGGCGAACCCAGG
	564	TTCCCGCGTAGCCAAACAGCTATA	TATAGCTGTTGGCTACGCGGGAA
	565	TTCGCGGATTGCTGCCGCATAACA	TGTTATGCGGCAGCAATCCCGCAA
	566	AAAAATGGCACCGAAGTTGAGGCA	TGCCTCAACTCGGTGCCATTTT
	567	CATTCCGCGAGTTGAAATCCAG	CTGGATTTCAACTCGCGCGGAATG
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	569	TGTCCATGACGTCGTTCTCTGGT	ACCAGAGAAACGACGTCATGGACA
	570	TCTCAGTCGGACTCGTATGCCAGA	TCTGGCATACGAGTCCGACTGAGA

	571	CTCCAAACGCACACATCAAGCATC	GATGCTTGATGTGCGTTGGAG
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	573	GGTGTGGAGGGTGGTGACCTCGA	TCGAGGTACCCACCCCTCCGACACC
	574	AGCGCTTGGTCATGATTGCAA	TTGCAAATCATGACCAAAAGCGCT
	575	CCGAGGACTTACGTCTGCCAGGA	TCCTGGCAGACGTAAGTCCTCGG
	576	GCCCAATCCAGTTCTATGCGCCC	GGGCGCATAAGAACTGGATTGGC
	577	CGGGTTAACCCACGCAAGTTATGA	TCATAACTTGCCTGGGTTAACCG
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	580	GCGCCACAAGATTACATGTCATT	AATGACATGTGAATCTTGTGGCGC
	581	GCCATGTTCAAGGGCCTTCGAAG	CTTCGAAAGGCCCTTGAACATGGC
	582	CGCGGTGTTGTCTAGGTGCCGG	CCGGCACCTAGACAAAACACCGCG
	583	CAACATTGTGGTGGCACTCCATCC	GGATGGAGTGCCACCACAATGTTG
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	585	GGCTATAAACGTGCGGACTGCTCC	GGAGCAGTCCGCACGTTATAGCC
	586	TGGGTAAATCACTATTGCGCGTT	AACCGCGCAATAGTGAATTACCCA
	587	GTCTTCATCGGCCCGCGCAAGCTA	TAGCTTGCCTGGGCCGATGAAGAC
	588	GCGACACACCCCTGTACTCTGATGC	GCATCAGAGTACAGGGTGTGTCGC
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	591	ACTCCGAAGCTTCGAGCGGCACGA	TCGTGCCGCTCGAAGCTTGGAGT
	592	TCCCGCCCACTAGACTGACTCGTA	TACGAGTCAGTCTAGTGGCGGGA
	593	ACCTTCTGGGTCGCTACCAATA	TATTGGTGAGCGACCCAGAAGGT
	594	ATCATCCCACGGCAGAGTGAAGAG	CTCTTCACTCTGCCGTGGATGAT
25	595	CGCTGGACTGGCCTATCGAGTCG	CGACTCGGATAGGCCAGTCCAGCG
	596	CGGTCTCAGCAACACTGTGCAAA	TTTGCAGACTGTGCTGAGACCG
	597	CGAACGTTCTCGATGTAATGCC	GGCCATTACATCGGAGAACGTTCG
	598	ATACCGTGCAGACAAGCCCCCTGA	TCAGAGGGCTTGTGCGCACGGTAT
	599	AGCTCATTCCGAGACGGAACACC	GGTGTCCGCTCGGGAAATGAGCT
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	601	ACTCGAACGGACGTTCAATTCCC	TGGGAATTGAAACGTCCGTTGAGT
	602	CTGCATGGTGGGTGAGACTCCC	GGGAGTCTACCCACACCATGCAG
	603	CCCGCAGTGTGGATGGCGTGTGA	TCAACACGCCATCCACACTCGCGG
	604	AATGTGTCGGCTTAAGCCGGGTG	CACCCGGCTTAGGACCGACACATT
35	605	TAAGACGAGCCTGCACAGCTGCG	CGCAAGCTGTGCAGGCTCGTCTTA
	606	GGCGTGGGAGGATAAGACGATGTC	GACATCGTCTTATCCTCCCACGCC
	607	TGCTCCATGTTAGGAACGACCCAC	GTGGTGCCTCTAACATGGAGCA
	608	CGGTGTTGGTCGGACTGACGACTG	CAGTCGTCACTCCGACCAACACCG
	609	CCGCGCGTATCTATCAGATCTGGG	CCCAGATCTGATAGATAACGCGCGG
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	612	TGCTTACGCAGTGGATTGGTCAGA	TCTGACCAATCCACTGCGTAAGCA
	613	ATGCAGATGAACAAATGCCGAAT	ATTGGCGATTTGTCATCTGCAT
	614	GCAATTCTGGGCCATGTATTGTC	GACGAATACTGGCCAGATTGC
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	616	GTGGAGCTAACGCGAGCCTCAGA	TCTGAGGCTCGCGATTAGCTCCAC
	617	TCGTAGTCTCACCGGCAATGATCC	GGATCATTGCCGGTGAGACTACGA
	618	TTATAGCAGTGCGCCAATGCTCG	CGAACAGTGCCTGTCGCTCAA
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	621	CATTAGCCCGCTGTCGGTAACGT	ACAGTTACCGACAGCGGGCTAATG
	622	GGAAAAGAAACTCAGACGCGCAATG	CATTGCGCGTCTGAGTTCTTC
	623	CGACTCGCTGGACAGGAGAACGT	ACGATTCTCTGTCCAGCGAGTCG
	624	CATGATCCTCTGTTACCCGCGG	CCCGGGGTGAAACAGAGGATCATG
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	626	AGTGATGCATCAGGCCGTATAC	GTATACGGGCCTGATGGCATCACT
	627	TATGGAAAGGGCAACAGCGCTATC	GATAGCGCTGTTGCCCTTCCATA
	628	CTGTGGTTGATGGAGGATCCACAC	GTGTGGATCCTCCATCAACCACAG
	629	ACTCGCTGGAATTGCGCTGACAC	GTGTCAAGCGAAATCCAGCGAGT
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	631	GGCGCAATGGCGCATAAACTA	TAGTATTATGCGCCATTGCGCC
	632	GGTCAATTGCGCTACATGCCCTA	TAGGGCATGTAGCGCGAATTGACC
	633	GATGGTGGACTGGAGCCCTCCGC	GCGGAAGGGCTCCAGTCCACCACATC
	634	CCGCGCATAGCGCAATAGGGGAGA	TCTCCCTATTGCGCTATGCGCGG
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	636	GCGTCGCAATTACCGGCCCTTA	TAAGGGCCCGTGAATTGCGAACGC
	637	TCGTTTCGGCTTGGAGAGTATCG	CGATACTCTCCAAGGCCGAAACGA
	638	AGGTGCAAGTGCAAGGCAGAGAGC	GCCTCTGCCCTGCACCTGCACCT
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	641	GTGTTGACGAAGAGCGAAATGT	ACATTCGCTCTTCGTCAAGCAC
	642	CAGTCCGTGCGCTTCATGCTCTCA	TGAGGACATGAAGCGCACGGACTG
	643	TACCGCGTAAGAGCCTACCCCGCG	CCGCAGGGTAGGCTTACCGCGTA
	644	GGCGAGTCTTGTGGGACATGTGT	ACACATGCCCCACAAGACTCGCC
35	645	CCAAAGCGAAGCGAGCGTGTCTAT	ATAGACACGCTCGCTCGCTTGG
	646	GCCGTAGGTTGCTCTCACCGAAC	GTTCGGTGAAGAGCAACCTACGGC
	647	AAATCCGCGATGTGCCGTGAGGCT	AGCCTCACGGCACATCGGGATTT
	648	GGCTTCGCACCCGTACCAATTAG	CTAAATTGGTACGGGTGCGAAGCC
	649	TGTAGAGTCCCACGTAGCCGGCAT	ATGCCGGCTACGTGGACTCTACA
40	650	CACTAGTCTGGGCAAGGTGCATT	AATGCACCTTGCCCCAGACTAGTG
	651	TGTACTCGGCAGGCCAATAGATT	AATCTATTGCGCCTGCCGAGTACA
	652	AACGGGTATCGGAAGCGTAAAGC	GCTTACGCTCCGATACCGTT

	653	CGGACTGCCGTTGCAAGTTGAG	CTCAACTTGCAAACGGGCAGTCG
5	654	ATCGTTAGCAGTGGAGCCCGTAA	TTACGGGCTCCAGTGCTGAACGAT
	655	ATGCATCGAACTAGTCGTGACGGC	GCCGTCACGACTAGTCGATGCAT
	656	TTCCAGGCATTAAGGAGAGGGAGC	GCTCCCTCTCCTTAATGCCTGGAA
	657	GTGCGACATCTACTCCACGATCCC	GGGATCGTGGAGTAGATGTCGCAC
10	658	CTCATCGTCCTAACACGAGAGCCC	GGGCTCTCGTGTAGGACGATGAG
	659	AATGGCACTTCGGCGGTGATGCAA	TTGCATCACC GCCGAAGTGCCATT
	660	CCGTGGGAGGGAATCCAACCGAGG	CCTCGGTTGGATTCCCTCCCACGG
	661	AAATTCTCGTTGGTGACGGCTCAT	ATGAGCCGTACCAACGAGAATT
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	663	TTAAGGATCAGGCGGAGCTTGCAG	CTGCAAGCTCCGCCTGATCCTAA
	664	CGCGACTAAGGTGCTGCAACTCGA	TCGAGTTGCAGCACCTAGTCGG
	665	GCTCGATTCACGGCCC GTTGTTC	GAACAACGGGCCGTGAAATCGAGC
	666	AGCAGAGTGC GTTGAGAGGCTAA	TTAGCCTCTGCAACGCACTCTGCT
20	667	TGGAGGTGAGGACGACGTGCACTA	TAGTGCACGTCGTCCCTCACCTCCA
	668	AACCGTTAGGGTACATT CGCGGT	ACCGCGAATGTACCC TAAACGGTT
	669	TATGATCGCTCGC TACAGTTG	CAA ACTGTGAGCCGAGCGATCATA
	670	GACTTTTGCGGAAACGT CATGGT	ACCATGACGTTCCGCAAAAGTC
	671	TGTCGGTTATTCCACCTGCAAGGA	TCC TTG CAGGTGGAATAACCGACA
25	672	CTATGGTTGCACTGCGCCGTGCA	TCGACGGCGCAGT GCAA ACCATAG
	673	AGCAGGGAAATCAATCGTCGCA	TGCGAACGATTGAATTCCCTGCT
	674	CCTAACCGAGCGCTTAGCATTCC	GGAAATGCTAAGCGCTCGGTTAGG
	675	CCCGACCC TAACTCGCATTGAATA	TATTCAATGCGAGTTAGGGTCGGG
	676	TTGCTTAATGGTGACGCCACGGAT	ATCCGTGGCGTACCAATTAGCAA
30	677	GATGCTCGCCGTGTTAGTCACG	CGTGA ACTAAACACGGCGAGC ATC
	678	TCGGATGACGAGTTCCATGACGG	CCGT CATGGAAA CTCGT CATCCGA
	679	ATGCGGTCTACTTCTCGATCGGG	CCCGATCGAGAAAGTAGACCGCAT
	680	TTGCGAGGCTAACGACACGGTAA	TTTACCGTGTGCTTAGCCTCGCAA
	681	AACTTAATTACCGCC TCGGCC	GGCGCCAGAGGCGGTAAATTAGTT
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	683	TGCGGATTACCGATT CGCTCTAA	TTAAGAGCGAATCGGTAAATCCGCA
	684	TGATAGGGGCCACGTTGATCAGA	TCTGATCAACGTGGCCCC TATCA
	685	TCGCTCCGTAGCGATT CATCGTAG	CTACGATGAATCGCTACGGAGCGA
	686	TGTCAGCTGGTAGCCTCCGTTGA	TCAAACGGAGGCTACCAAGCTGACA
40	687	AGCGTCGCATGACGCTTACGGCAC	GTGCCGTAGCGTACGCGACGCT
	688	TCACTCAGCGCTGTGACTGCCTGA	TCAGGCAGTCACAGCGCTGAGTGA
	689	GTTTGCCTATAGTGGGGACCGT	ACGGTCCCCACTATAGCGCAAAC
	690	GTCGCATTCTGCACTGGCTT CGCC	GGCGAAGCCAGTGCA GAATGCGAC
	691	TGATTAGGTGC GGTC CGT TAGTCC	GGACTACGGGACCGCACCTAATCA
	692	AAGGGACCTTGGGTGACGGCGAGA	TCTCGCCGTACCC AAGGTCCCTT
	693	TCAAATGGCCACCGCGTGTCA TTC	GAATGACACGCGGTGGCCATTG A

	694	CTCCGACGACCAATAAAAGCCGC	GCGGCTATTATTGGTCGTGGAG
5	695	GGCTATTCCCCTAGAGAGCGTCCA	TGGACGCTCTACGGGAATAGCC
	696	TGGATAACCTCTCGGCCATCCAC	GTGGATGGACCGAGAGGTTATCCA
	697	GACCGCTGTACGGGAGTGTGCCTT	AAGGCACACTCCCGTACAGCGGTC
	698	GCCACAGAGTTTAGCAGGGACCC	GGGTCCTGCTAAAACCTGTGGC
	699	CCCACGCTTCCGACCCTGACCT	AGGTCACTGGTCGAAAGCGTGGG
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	701	AGCCACTCGACAGGGTCCAAGC	GCTTGGAACCCCTGTCGAGTGGCT
	702	CAGGATGAGCAAAGCGACTCTCA	TGGAGAGTCGCTTGCTCATCCTG
	703	CAAGGTATGGTCTGGGCCTAAGC	GCTTAGGCCCGACGACCATACCTG
	704	GGTGGTCGGCCTAAACTCTTCGG	CCGAAAGAGTTAGGCCGAAACACC
	705	TTTAGTCGGACCCCTGTCGGCAATT	GAATTGCCACAGGGTCCGACTAAA
	706	CACACGTTCCGACCAGCCTGAAC	GTTCAGGCTGGTCGAAACGTGTG
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	708	TTCACAACTCGCCGAAAAGTGCACC	GGTCAGTTTCGGCGGATTGTGAA
	709	AACAGGATATCCGCGATCACGACA	TGTCGTATCGCGGATATCCTGTT
	710	TACGTCGGATCCATTGCGCCGAGT	ACTCGCGCAATGGATCCGACGTA
	711	CATGGATCTCGGTTGATCGCC	GGCGATCAAACCGAGAGATCCATG
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	713	ATTGGCACGTGTCGTGCCATGTT	AACATGGCACGACACGTGCCAAAT
	714	CCCGCGTTGACCACTTGAGGTGC	GCACCTCAAAGTGGTCAACCGGG
	715	TTGGACGTGACAAGCATGGCGCTC	GAGCGCCATGCTTGTACGTCCAA
	716	CTGAATCGCGCAAGTAAATGGGGG	CCCCCATTACTGCGCGATTCAAG
25	717	GATAAGGTCCACCAGATTGCGCGC	GCGCGCAATCTGGTGGACCTTATC
	718	CTAACAAATTGCCAACCGGGACGGC	GCCGTCCCGGTTGGCAATTGTTAG
	719	GGTAACCTGGGTGCTTGAGGTTA	TAACCTGCAAGCACCAGGTTACC
	720	ATCGGAGCCACCATTGCGATTGGG	CCCAATGCGAATGGTGGCTCCGAT
	721	GTGAACTGGCTTGGCCAGGAGTTA	TAATCCTGGGGCAAGCCAGTTAC
30	722	AGGCAGATAGCATGGTCCCATAATGA	TCATATGGGACCATGCTATCGCCT
	723	AACGGTATCGTGGCTAATGCACGA	TCGTGCATTAGCCACGATACCGTT
	724	AGTAGTGGCCTCCAGATCGGCAA	TTGCCGATCTGGAGGACCAACTACT
	725	CCGTTGAATTGGACGGGAGGTTAG	CTAACCTCCCGTCCAATTCAACGG
	726	GCATAAGTGGCGATCGCGAAGGG	CCCTTCGCGATGCCGACTTATGC
35	727	CGACAAGATGCAGCTGCTACATGC	GCATGTAGCAGCTGCATTTGTCG
	728	TCGCAGTGTACCGACCGATAAG	CTTATCGGTGGGAATCACTGCGA
	729	CAAGGCGAGTCCACTCGAGGGGAC	GTCCCCCTCGAGTGGACTGCCCTG
	730	GCAACTTGACGGCATAAGTGGCC	GGCCACTTATGCCGTGCAAGTTGC
	731	TCCGAGCTTGACGTTCGCGACGTC	GACGTGCGAACGTCAAGCTCGGA
40	732	AGCGCTGGCTGTGCTGCCATCTC	GAGATGGCAGCACAGCCCAGCGCT
	733	TTCATGTCGCTGAGTAACCTCGC	GCGAGGGTTACTCAGCGACATGAA
	734	CGAACCGCTAATGCCATTGTCAG	CTGACAATGGGCATTAGCGGTTCG

	735	CACGGAAAGGTGGGACAATGCCG	CGGCGATTGTCCCACCTCCGTG
	736	CACAGATGGAGACAAACGCGCCTT	AAGGC CGCTTGCTCCATCTGTG
5	737	TTTCGCAACTCGCTCCATAACCC	GGGTTATGGAGCGAGTTGCGAAA
	738	ACGTTACGTTCCGGCGCTCTAA	TTAGAGGCGCCGAAACGTAACGT
	739	TATCGGATTGCGTGGGTTCAATC	GATTGAAACCCACGCAATCCGATA
	740	CTTCCACAAATTGTCGCGACGCAC	GTGCGTCCGAGACAAATTGTGGAAG
	741	TGCACAAAGGTATGGCTGTCCGGC	GCCGGACAGCCATACTTGTGCA
	742	TCCGATGCCAGTCCCATCTTAAGA	TCTTAAGATGGGACTGGCATCGGA
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	744	CGGTGTTCCCGTGTGAAAAAT	ATTTTTTCGACACGCGGAACACCG
	745	TCTAGCAGGCCTTTGAATGCCA	TGGCGATTCAAAAGGCCTGCTAGA
	746	GAGTCACCTCTGAGACGGACGCCA	TGGCGTCCGTCTCAGAGGTGACTC
	747	TCTTCTGTCATCCTGCAGCAGCAT	ATGCTGTCAGGATGACAGAAGA
	748	GC GGATGAAACCTGAAAGGGCCT	AGGCCCCTTCAGGTTCATCCGC
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	750	GCATTGGCTTCGGATTCTCTACA	TGTAGGAGAATCCGAAGCCAATGC
	751	AGGCGGCCAACCTGTGAGGTCTG	CAAGACCTCACAGTTGGCCGCCT
	752	ACACCATGTGCTCCCGCCTGCAGT	ACTGCAGCGCGGAGCACATGGTGT
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	754	CTGCATCCCTGTAGCAGCGCTCCG	CGGAGCGCTGCTACAGGGATGCAG
	755	GTGCCGTATTCGACCTGTGCGTT	AACGCACAGGTGAAATACGGCAC
	756	GCAGTGCCTACTTCAGTTAAAAG	CTTTGAACTGAAGTGCCTACTGC
	757	GCGATTTAACGCGATGCCCTGACG	CGTCAAGGCATCGCTAAAATCGC
	758	TAGGTGACCTAGGCTTGCTTGC GG	CCGCAAGCAAGCCTAGGTACCTA
25	759	CTGGATACCTTGCCTGTGCGGCGC	GCGCCGCACAGGCAAGGTATCCAG
	760	CCCCTTACGGCTCGTCGTCTATGC	GCATAGACGACGAGCCGTAAGGGG
	761	GCGCTTGCCCGATGCGATGCATTA	TAATGCATCGCATGGGCAAGCGC
	762	TTTCTGTAAGCGGCCCTGGGTTCA	TGAACCCCAGGCCGTTACAGAAA
	763	GGCTGAGGTGAGCGGTAGGATGA	TCATCCTTACCGCTCACCTCAGCC
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	765	GGAGGTAACGCCGTGTACGTAGGA	TCCTACGTACACGGCGTTACCTCC
	766	GTAATCCATTGTGGCTGCGTCAA	TTGACGCAGCCACAAATGGATTAC
	767	CAAACCCATTCCAGCAGACGCCCTG	CAGGC GTCTGCTGGAATGGGTTG
	768	TAGGAGGAATTGGCATGCCGGCG	CGCCCGCATGCCAAATTCCCTCTA
35	769	ATAGGTAGGATGTGCCCGCGTTG	CAACGCCGGGCACATCCTACCTAT
	770	GCAAGTGCTTAGCTCGTCAGCCTC	GAGGCTGACGAGCTAAGCACTTGC
	771	CTGGCTGTGCGCATCTCGTTAAC	GTAAACGAGATGCGACACAGCCAG
	772	CTAACGTGCTCGCGCAATCACT	AGT GATTGCGCGAGACGACGTTAG
	773	TTTCATAAACGTTGCCCCGAGC	GCTCGGGGACAACGTTATGAAAA
40	774	AGCAGGAGGACGAAACCTCCGCTCC	GGAGCGGGAGGTTGTCCTCCTGCT
	775	TTCAAGCACCATCGTGCATCCAA	TTGGATTGCACGATGGTGTGCTTGAA

	776	AGCGTCGCCAGTGATCGCTAGTGG	CCACTAGCGATCACTGGCGACGCT
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	778	CGCTTCGCGTATTCACTAGCGGTT	AACCGCTACTGAATAACGCGAAGCG
	779	TCGGACCGCTGACACTCATTATA	TATAATGAGTGTGACCGTCCGA
	780	TCTGAGCAGGCCAGCGCTCCAGCT	AGCTGGAGCGCTGGCCTGCTCAGA
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	782	AGTTTCGCCCTGATGCGTCGGTG	CACCGACGCATCAAGGCAGAAACT
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	785	ATTGGCCGAGGGTGAATGCAGCCT	AGGCTGCATTCACCCCTGGCCAAT
	786	TGATCCATCCGAATGCTTTCCAT	ATGGAAAAGCATTGGATGGATCA
	787	GCACACAGTTGCTTGGCCATGA	TCATGGGCAAGACAACGTGTGTC
	788	CTGGCGGGCAGTGGAAAAAACAC	GTTGTTTTTCCACTGCCGCCAG
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	790	TCTCCTCTCGTCGAGTCGTGGA	TCCACGAAC TGCGACGAGAGGAGA
	791	TAGCGTATTCACTCTGCCGAGCA	TGCTCGCAAGAGTGAATACGCTA
	792	CAATCAAAGCCACGGCGCATGG	CCATCGCGCCGTGGCTTTGATTG
	793	AGCGTCACCGAACAGCAGATCT	AGATCTGCTGAATTCCGTGACGCT
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	795	TAGGCACTGCCGGTTAGATTCAA	TTGAATCTGAACCGGCAGTGCCTA
	796	AACAGGGTGATAACGGTGGCCAAT	ATTGGCCACCGTTATCACCTGTT
	797	CGTGCCTACCATGTGTAAGTGCCT	ACGCACTACACATGGTACGCACG
	798	GACCAATTCTACTTCGGCAGCCC	TGGGCTGCCGAAGTAGAATTGGTC
25	799	ATCGGACCGATTGCTTTGGCTG	CAGCCAAAAGCAAATCGTCCGAT
	800	TCCGCCGAAGCACACGTTATTG	CGAATAAGCGTGTGCTTCGGCGGA
	801	AACGGTACGCATTGTGAGCAGTGT	ACACTGCTACAATGCGTACCGTT
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	803	CAGAGGGGACAGCCGTATGCCCTA	TAAGGCATA CGGCTGTCCCCCTTG
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	805	TTGGCCTCCGACCTACGACATAT	ATATGTCGTGAGGTGGAGGCCAA
	806	CGTTTCGCTAGCATCTGGCGCCGA	TCGGCGCCAGATGCTAGCGAAACG
	807	ACTAACCGGTGGAGCCGGTGGATG	CATCCACCGGCTCCACCGCTTAGT
	808	ATATTGGCTGCGTTACGGGCCGC	GC GGCCCGTAAACGCAGCCAATAT
35	809	CCGCTATGGTGGCAATCCGATAC	GTATCGGGATTGCCACCATAGCGG
	810	GTTGCATGTGGCTCAGGGCATA	TATGCCGCTGAGCCACATGCAAC
	811	ATTCTGGGAGTGACCCAGGGCTT	AAGCCCTGGGTCACTCCCCAGAAT
	812	CTCTCCAAGGAGACGAGCCAATGT	ACATTGGCTCGTCTCCTTGGAGAG
	813	GAAAGGACGGATTGGGGCTAA	TTAGCCCCAAATCCGTCTTTC
40	814	TATGTAGTACCTGGCTCGCGCCA	TGGCGCGAGCCAAGGTACTACATA
	815	TCCCTTCGATGAGCGGCTGTACT	AGTACAGCCGCTCATCGAAAGGGA
	816	TAGATCGGGCAGAGCCGTATCTT	AAAGATA CGGGCTCTGCCGATCTA

	817	GGAATGCTTAGGCTGCCGAGCTG	CAGCTGGCAGCTAAAGCATTC
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	820	ATGTTGCTAGTGCCTTCGGGCCT	AGGCCCGAAAGGCAGTAGAACAT
	821	CCAATGTGCGCAGACTCAGTCATT	AATGACTGAGTCTGCGCACATTGG
	822	GATAGTGCTCGCAAACGGGCCTTC	GAAGGGCCCCTTGCAGGCACTATC
	823	GCACCCCTGTTGCCTCATTGAGCGT	ACGCTCAATGAGGCAACAGGGTGC
	824	GGCGTGAATAGAGTGACCAGGCGG	CCGCCTGGTCACTCTATTACGCC
	825	ACGTGCCAGCTGCCGGCACTTTAT	ATAAAGTCCCCCAGCTGGCACGT
10	826	AGTGGAAATAGTCGCGTCGTGCCGC	GCGGCACGACGCGACTATTCCACT
	827	ACTCGCCTATTACCGCTGGATTGG	CCAATCCAGCGTAATAGGCGAGT
	828	GAGACCGGATTGAGATGATCCCGT	ACGGGATCATCTCAATCCGGTCTC
	829	CTGGCAGTTTACCAACCGAACAGT	ACTGGTTCGGTGGTAAACTGCCAG
	830	TTACATTGCCGATTCGCATGTGA	TCACATGCCAAATCGCAATGTAA
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	833	AAGACCGAACGGTCTCTGAGGGC	GCCCTCAGAGAGACCTCGGTCTT
	834	GCCTATGGCTCCAGCTCAGCAGTA	TACTGCTGAGCTGGAGCCATAGGC
	835	CGTATCATAGCGTTGGTGGACAA	TTGTCCACCGAACGCTATGATAACG
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	837	TGGGCAATTCGAACGTCGGTCT	AGACCGACGTTCCGAATTGCCCA
	838	TTGCGGAGATGCGACGGTACATTG	CAATGTACCGTCGCATCTCCGCAA
	839	ACTTCGACGTGATCTGGACTG	CAGTCCAGATCGACGTGCGAAAGT
	840	CTAACTGCCCGGGCAAACGTATTA	TAATCAGTTGCCCGGGCAGTTAG
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	842	GAATTGGAACGGTGTCCGATGA	TCATCGAACACCGTCCAAATT
	843	GTCCATCCATCTACGGCATCAGGA	TCCTGATGCCGTAGATGGATGGAC
	844	TAAACGACCTGGCACATGTGCGTA	TACGCACATGTGCCAGGTGTTTA
	845	CACCATCCAAGAGCCAATCTAGG	CCTAGGATTGGCTTGGATGGTG
30	846	ACTCATATACGATCAGTCCGCCGC	GCGCGGGACTGATCGTATATGAGT
	847	GTGCCAACCGACGATCAACCGAAC	GTTCGGTTGATCGTGGTGGCAC
	848	TGGGGTTCGTACAGGTGGTTCAT	ATGAACCGACCTGTACGAACCCCA
	849	AACAGTAGAGGCAGGGCTGCCGG	CCCGCAGGCCCTGCCCTACTGTT
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	853	CACACGTACACCATCCAAAGTGG	CCACTTGGATGGTGTGACGTGTG
	854	ATGCTCAGGTGCTAAATACGGCCA	TGGCCGTATTTAGCACCTGAGCAT
	855	AAAAATGTTAGCGCGCTGACTGG	CCAGTCAGCGCGCTAAACATT
40	856	ATAGTCCGTTCCGTTCCAACGA	TCGTTGGAACGGAAACGGACTAT
	857	TCGATCTCTGGTTGCAGACCAG	CTGGTCTGCAACCCAGAAGATCGA

	858	GTCGGCGCAGCCGATCCTCATGTC	GACATGAGGATCGGCTGCGCCGAC
	859	GTTCGGGGTGTGAAAAGGATCT	AGATCCTTTGACACCCCGCAAC
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	861	TGATGTGCGTTTCAGCTTCGCG	CGCGAAAAGCTGAAACGCACATCA
	862	GTAAAGGGGTGAGAACATCCGGCC	GGCCGGATGTTCTCACCCCTTAAC
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	864	CCGACCTAATAAGGGCAACAATG	CATTGTTGCGCCTTATTAGGTGG
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	867	TGGTACTCCTTGTATGCCTGCCA	TGGCAGGCATGACAAGGAGTACCA
	868	GGCACAGGTTCTTGCAGCGCGG	CCCGCGCTGCAAGAGAACCTGTGCC
	869	GAATCTGGCATTGCTACGAGACC	GGTCTCGTAGCAATGCCAGATT
	870	CGAAATGGGAGCGTCCACTACCAC	GTGGTAGGGACGCTCCCATTTCG
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	873	GAGGGTCCCTGCTCAGAGTTGGTT	AACCAACTCTGAGCAGGGACCCCTC
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	875	CTACCCGAATGGATTGCGGATGGC	GCCATCCGCAATCCATTGGGTAG
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	877	TAACGATCCATTCCACGAATGCAG	CTGCATTGTGGAATGGATCGTTA
	878	GGCCGCACGTACGATTACGCCCTG	CAAGGCAGTAATCGTACGTGCGGCC
	879	TGGGAATGCATCAGTTGGCT	AGCCAACAACGTGATGCATTCCCCA
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	883	TGCATGCGAGCAAATAACCCGGAC	GTCCGGTTATTGCTCGCATGCA
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	887	GGCTCCCGCGATAACGTAATTGCG	GCGAATTACGTTATCGCGGAAGCC
	888	TGTAGCCGACTAGGGCGAAGCCC	GGGCTCGGCCCTAGTCGGCTACA
	889	AAGCGAACGCCCTGGCTGAATATT	AAATTCAGCCAGGGCGTCGCTT
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	892	CCCCACACGTTGCGCCTATATGTG	CACATATAGCGCAACGTGTGGGG
	893	GGCGGGCACAACCAACACAGATG	CATCTGTGTTGAGTTGTGCCGCC
	894	CGACTGCGGGATCACCGGTGATTA	TAATCACCGGTGATCCCGCAGTCG
	895	TCGGGACATGACCGGTACGGAGTC	GACTCCGTACCGGTATGTCCCAG
40	896	TACCTCGAGTGGCCGTTGATCGGG	CCCGATCAACGGCCACTCGAGGTA
	897	TAATTGTCAGGGCTAGCCGAACCA	TGGTCGGCTAGCCCCATGAATTA
	898	ACACTCTAACGCCGATTCGTTCGA	TCGAACGGAATCGGCTAGAGTGT

	899	GTGGGCGTGAGTGACACGCACAAA	TTTGTGCGTGTCACTCACGCCAC
	900	ACGACTCCTCGGGCAAAGTACGTA	TACGTACTTGCCTGGAGGAGTCGT
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	904	GGTACTTCCGGCGTATCGGGCAC	GTGGCCCGATA CGCCGGAAGTACC
	905	GTGGGTTTGTTCACCTCTGGG	CCCAGAAGGGTGAACAAAACCCAG
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	908	GTGAAATGGATCCAGAGAGGGCCA	TGGCCCTCTCTGGATCCATTTCAC
	909	TATAAACGCTGCAGGGCTCCGTTA	TAACGGAGCCCTGCAGCGTTATA
	910	GTTATTCAAGGCGGCTTGTAAACGGG	CCCGTTACAAGCCGCTGAATAAC
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	913	CCGTCTTCAGGACAACGGTATCG	CGCATACCGTTGCTGAAGACGG
	914	GGACCCCTTGACAGATTGCGGCAC	GTGCCGCAATCTGTCAAAGGGTCC
	915	TAAATTTATGCCAGGCGGCGCT	AGCGCCGCCCTGGCGATAAAATTAA
	916	GCCGAACGCAAGATCGCTTGA	AGTTCAAGCGATCTTGCCTCGGC
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	918	CAAACCACAGCTTACAGGCTCGT	ACGCAGCCTGTAAGCTGTGGTTG
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	920	TAGCGCGCATCACACTTGAATCG	CGATTCCAAGTGTGATGCGCGCTA
	921	TGCTGACACAAACGAGCCGTTCG	CGAAACGGCTCGTTGTGTAGCA
25	922	CGCTTAACGGCATTGACTGTCCAC	GTGGACAGTCATGCCGTTAAGCG
	923	TTCCACGGCCGTGTATTACGGATA	TATCCGTAATACACGGCCGTGGAA
	924	TTTATGCCATTGGCCAGGAAGACT	AGTCTCCTCGGCAACGGCATAAA
	925	AGTGCCGAGATAGGGACTGGCG	CGCCCAGTCCCCTATCTGGCACT
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	929	ATATGCGTCACCACCCGGTCCGA	TCGGAACCGGGTGGTGACGCATAT
	930	CCATCAGTAAGGGTTGCTGCCA	TGGCAGCAACCCCTCACTGATGG
	931	CATATGTGCTTGGCTGCGATGAC	GTCATCGCAAGCCAAGCACATATG
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	933	CGATTGGTCAAGAAGCGGAAAT	ATTCCGCTTCTTGACCAAATCG
	934	ATCAGAGGCCCTCCGCCTCGTTA	TAACGAGGCCGGAAAGGCCTCTGAT
	935	ATTGTTGCGTTGCCACATCGCAG	CTGCGATGTGGCAACGACAACAAT
	936	TGAAATGTGCTGGACGCGAGTCT	AGACTCGCGTCCAGACACATTCA
40	937	GCGGGCGATGCTCCTAAAGGGTA	TACCCCTTAAGGAGCATGCCCGC
	938	CCGCAATCTCCATGCGTCGACCGT	ACGGTCGACGCATGGAGATTGCGG
	939	TGCCGCGTAATCACCTGGAACTTG	CAAGTTCCAGGTGATTACGCGGCA

	940	TTCAGTAGCCAGCGGTAGTGTGA	TCACACTACCGCTGGCTACTGGAA
5	941	CTGAATTCGCCTATTGTCGGCA	TGCCGAACAATAGGCGGAATTCAG
	942	GCTTGAACTCGAGGCGATGTTCT	AGAACATCGCCTCGAGGTTCAAGC
	943	CAAGCGTGGAAAGTACGACCCGCCA	TGGCGGGTCGTACTCCACGCTTG
	944	GTGTGCACTGGATCCGAGCCCTAG	CTAGGGCTCGGATCCAGTGCACAC
	945	TCCCTGGGCTAGCATTGCGAGGTT	AACCTCGCAATGCTAGCCCAGGGA
	946	AGAACCAAAGACGCTTGTGCG	CGGCAAACAAGCGTCTTGGTTCT
	947	CGTCACATGCAAACGTTCCCTCCC	GGGAGGGAACGTTGCATGTGACG
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	949	GCGGGCCCAATGAGTATCCGTCAT	ATGACGGATACTCATTGGGCCGC
	950	TAGTGACTGTGAACGCCCCCTGGTT	AACCAGGGCGTTCACAGTCACTA
	951	GGCACCGTCTGCCGCCGTATATC	GATATA CGCGCGGAGACGGTGCC
	952	TCGATGCAGTCTTTTCCCCTCAA	TTGACGGAAAAAGACTGCATCGA
	953	ACCCCGTGGGTTTCGCCATTIT	AAAAATGGCGAAACCCCACGGGTT
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	955	CGCAGCGACCTCATCTCTGGAGCC	GGCTCCAGAGATGAGGTCGCTGCG
	956	CGACCCAGCACTCCTAAAATCGGT	ACCGATTTAGGAGTGCTGGTCG
	957	ACGCGCCGCTCATCACTACAATCT	AGATTGAGTGTGAGCGGCCGCGT
	958	CGCAACTTCCGTGGCAAAGCCAG	CTGGCTTGCACAGGAAGTTGCG
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	960	CCGTTGTAATTGCCATTCTCCGT	ACGGAGAATGGCAATTACAAGCGG
	961	GTAACCAGGGAGTCCTGGCTGTG	CACAGCCCAGGACTCCCTGGTTAC
	962	AGCGCAAGATCTGGGGCAGTCAC	GTGACTGCCCTCAGATCTTGCCT
	963	GCGTACATCTGCTCATCAGCATGG	CCATGCTGATGAGCAGATGTACGC
25	964	CCTCTGTGGCAGGAAAGAAACCGT	ACGGTTTCTTCCCTGCCACAGAGG
	965	CCTATGCAATGGACCTGCATCGGA	TCCGATGCAAGTCCATTGCATAGG
	966	CTCGGTGGATGGCGAATAAGGATA	TATCCTTATTGCCATCCACCGAG
	967	CCTCACTCGTGTGGCGTGACGCA	TGCGTCACGCCATCAGAGTGAGG
	968	TACGCTCACAGAACGCCATACGCC	GGCGTATGGCGTTCTGTGAGCGTA
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	971	ACTTCAGCACGCGAACAGCGCAA	TTGCGCTGTTCGCGTGCTGAAAGT
	972	CTAAACGCCCTTGATGCATGAGCA	TGCTCATGCATCAAGGGCGTTAG
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	975	TAGCCGCGCGGCTCTATGCTCTT	AAGAGCATAGGAGCCCGCGGGCTA
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	977	TGAGCTGCCTGCCACGATGCCCTC	GAGGCATCGTGGCAAGGCAGCTCA
	978	CCGCCGTATACGTGCCATAGTTG	CAAACATGGCACGTATACGGCGG
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	1022	TTGGTGAACCTGGCCGTCGGAAG	CTTCCGACGGGCCAGTTACCAA
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	1029	ACCCCTAAAGCAATAGGCGGCG	CGCCGACCTATTGCTTAGAGGGT
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	1033	TGTCGCCCCATGGCAGGTTAACAC	GTATTTAACCTGCCATGGGCGACA
	1034	GGGGGCCCATCAATTCTATTATCGA	TCGATAATGAATTGATGGGCCCCC
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	1039	TCAACGCACTGGCGATGACTAGAT	ATCTAGTCATGCCAGTGCCTTG
	1040	CGGGAAATGTCTTAGCCGTGAA	TTCGACGGCTAAAGACATTCCCG
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	1042	GGCCTGTTCTGTCCAACCTGGGCT	AGCCCAGTGGACAGAACAGGCC
	1043	ATTCACCTCGCTGATCGCTTCCG	CGGAAGCGATCAGCGAGGTGAAAT
	1044	AGTGACGCCAGTCGCGAGGGTTA	TAACCCCTCGCAGTCGGCGTCACT
	1045	AGTTGTCATCCTGTCGGGACC	GGTCCCGGACAGGATGAGACAAC
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	1048	ATGCGATCCATGACAAGGGTTGCT	AGCAACCCCTGTCATGGATCGCAT
	1049	CCCGTGGAGATGATGTGCGGCTTA	TAAGCCGCACATCATCTCCACGGG
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	1058	ATCGGAAGTGCTGACTGACACACG	CGTGTGTCAGTCAGCACTCCGAT
	1059	CCTCAGACCCCTATCTGGGTTGACG	CGTCAACCCAGATAGGGTCTGAGG
	1060	CTGTGTGGCTGGTCCGGCTGTC	GAACAGCCGGACCAGACCACACAG
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	1062	ACAGGCACGTAAGTGCTCAATCGG	CCGATTGAGCACTACGTGCCTGT

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	1082	CACCAGCCTTACGTGCGGCGTTAA	TTAACGCCACGTAAAGGCTGGTG
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	1102	ATGTCCACCGAGTGCCTCCGATATC	GATATGGACGCACTCGTGGACAT
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40			

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	1107	CTTATCCCATGTGCCGGTCTGACT	AGTCAGACCGGCACATGGATAAG
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	1117	ATCCGCTGGCGCTTGACGAAGAA	TTCTCGTCAAAGGCCAGCGGAT
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	1120	TCGATCCCGCGATCTGGCTATTG	CAATAGGCCAGATCGCGGGATCGA
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	1122	TCACACACCAACTGCCACAGATG	CATCTGTGCCAGTTGGTGTGTA
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	1124	GACATTTAACCGACCGATTGTGC	GCACAATCGGTGGTTAAATGTC
	1125	GGCACCGAGCCAGTAGGCCTCTGA	TCAGAGGCCACTGGCTCGGTGCC
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	1140	CCTCGCTAGAGAAATCCACGGGAT	ATCCCCTGGATTCTAGCGAGG
	1141	TAACATCGGTGCAAACCGTGGCGC	GCGCCACGGTTGCACCGATGTTA
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	1208	CCAGAGAGGCCGGCTACTGACTCA	TGAGTCAGTAGCCCGCCTCTCTGG
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	1218	ATGCATCCAGCGTCCCCCTGATTA	TAATCAAGGGGACGCTGGATGCAT
	1219	ACCGTCATCAGTCGCAGGCTCTG	CAGAAGCCTGCGACTGATGACGGT
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	1221	TTAACATTGGACCCAGGACCTGG	CCAGGTCTGGGTCCGAATGTTAA
	1222	TGGTGTGAAACTCCCTTGCCTGTT	AACACGCAAGGGAGTTGACACCA
	1223	TACTCCAGTCGCCTGCGCGAAC	GTTTGCAGCAGGGACTGGAGTA
	1224	CGCAATGCCGTAAGCATGCCAAC	GCTTGGCATGCTTACGGCATTGCG
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	1226	ATGTTGCACGCGCACTGTATCACA	TGTGATACTGCGCGTGCAACAT

	1227	ATCGCCTAACTACCCGCGCGTGC	GCACGCCGCGGGTAGTTAGGCAT
	1228	TGGCCAGGAAACACAAGCTCGTA	TACCGAGCTTGTGTTCCCTGGCCA
	1229	AAACATGGGTGCGTCTGAGATCA	TGATCTCAGACGCGACCCATGTT
5	1230	GCGAGAGCTGCGATTCCCTTTAG	CTAAAAGGGAATCGCAGCTCTCGC
	1231	CCGGCCAAACAAGAGACGAGCGGA	TCCGCTCGTCTCTTGTTGGCCGG
	1232	AATGGGGCACAGTCTCGCTTGACA	TGTCAAGCGAGACTGTGCCCCATT
	1233	TGTCTCGGGCCTTCAGGACACACT	AGTGTGTCTGAAGGCCGAGACA
	1234	TCCACCTTCATTAAGTGGTCGGC	GCCGAACCACCTAACATGAAGGTGGA
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	1236	GAGCCGATGGCTATCGTCGTCGG	CCGACGACGATAGCCCATCGGCTC
	1237	CACGAATTACGCACGCACAGAGGA	TCCTCTGTGCGTGCCTAACATCGT
	1238	GCTGTGACGCTCCCTCAACTAGG	CCTAGTTGAGGGGAGCGTCACAGC
	1239	CGCTCTGAAAACGCGGGCTACGTT	AACGTAGCCCACGTTTCAAGAGCG
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	1241	CCAACCCCAGTGTAGCGCAAATG	CATTGCGCCTACACTGGGTTGG
	1242	GAAGTAGGGGATGTTGGCCGGCG	CCGCCGGCCAACATCCCCTACTTC
	1243	CAACGTGGCACCTGTTTAGCAG	CTGCTAAAACAGGTGCCACGTTG
	1244	CTAGCTGCGATCCGAACCTCTACG	CGTAGAGGTTCGGATCGCAGCTAG
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	1246	AGACTGGCAATTTCGAGGCCAA	TTGGCCTCGAAAAATTGCCAGTCT
	1247	CTGGCCGTCCATGAGTTGGTCAG	CTGGACCAACTCATGGACGGCCAG
	1248	CATGCTGAAACACGGGATTGCCAT	ATGGCAATCCCGTGTTCAGCATG
	1249	CGATATGTAAGACAGCCGTCGCAA	TTGCGACGGCTGTCTTACATATCG
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	1251	GTTCGAACCCCGCGATGTTAAATG	CATTAAACATCGCGGGGTTCGAAC
	1252	GTTGTTAGGAGGCTCGAGGCTGCT	AGCAGCCTCGAGCCTCTAACAAAC
	1253	ACTGGTGCTACGCGGGATATTGA	TCAAATATCCCGCGTAGCACCAGT
	1254	CTGGGAGCTATCCTCAGCCGAATC	GATTGGCTGAGGATAGCTCCCAG
	1255	GAACTCGCCGCTGCCAAGGGTAG	CTACCCCTTGGCAGCGGGAGTTC
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	1258	CTAAGGTCAAAGCGCTGTCGCCAG	CTGGCGACAGCGCTTGCACCTTAG
	1259	CCGTAGCGGTGCTCGACCAGGTT	GAACCTGGTCGAGCACCCTACGG
	1260	TGGGGACGAATCGAATGTAGTGA	TCACTACATTGGATTGTCCTCCA
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	1262	CTTTCGCGGGTGGTCAATAAAAG	CTTTTATTGACCACCGCGCAAAG
	1263	CTCGGGGATGCCCTTGGCATTA	TAATGCCAAGAGGGCATCCCCGAG
	1264	CGAAACGTGGTGCAGAACCTGAA	TTCAAGGTTCTGCACCACTGTTCG
	1265	GGAGTTACGAGTCGAGCAGTCGC	GCGACTGCTCGACTCGTGAACCTCC
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	1267	TGGCTGGACATTGTCGCAATGCA	TGCATTGCAAGACAATGTCCAGCCA

	1268	ATCGGCTGCCTCAGCCCTAATT	AAATTAGGGACTGAGGCAGCCGAT
	1269	CCAGCATGGAGTTAAGTGAGCGCG	CGCGCTCACTTAACCTCATGCTGG
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	1271	CGAAATCGCACAGGAATTGCGTC	GACGCAATTCTGTGCGATTCG
	1272	GGCAATTTCGGGACACTCGTTCA	TGAAACGAGTGTCCCAGATTGCC
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	1274	CCCAGCTAACCTCAGCTGGCTGT	ACAGCCCAGCTGGATTAGCTGGG
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	1277	GCACGGGGTCTCAATGCTTAGGGT	ACCCTAACGATTGAGACCCGTGC
	1278	GCGCAACAAGTAGCCTACCGAGGC	GCCTCGGTAGGCTACTTGTGCGC
	1279	TAGCAGGCTGATGCCGTACACAC	TGTGTAGACGGCATCAGCCTGCTA
	1280	GCAAGCGGCATCGTACAACCTGT	ACAAGTTGACGATGCCGCTTGC
	1281	GCACCTCTGGTAAGCCTGAAAGGG	CCCTTCAGGCTTACCAAGAGGTGC
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	1284	GATATTGGGTCCGGCGCGCATTAC	GTAATGCGGCCGGACCCAATATC
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	1286	AACCTTAGTGCAGCTAGGTGGGGT	ACCCACCTAGCCGCACTAAGGTT
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	1289	TTCTGACAACATCGACCCCTGGCTC	GAGCCAGGGTCGATTTGTCAGAA
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	1291	GTACTCTGTGCAACGGTCCCAGT	ACTCGGGACCGTTGCACAGAGTAC
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	1295	CTTAGAGGGACGAGGCCATGAATG	CATTGCGCTCGTCCCTCTAAG
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	1300	TCAGGAAAGGCCTAAAGGCAGAAAG	CTTCGCCTTAAAGCCTTCTGA
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	1304	CTCACTCATTGATTGCCGCGG	CCGCGGGCAATCAGAATGAGTGA
	1305	GGGGTGATCTCTCGAACGTCACCC	GGGTGACGTTGAGAGATCACCC
	1306	AAGGTTGCTGCTAGCGTACCTCGA	TCGAGGTACGCTAGCAGCAACCTT
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	1308	GTTGGACCTGTTGGGAGTGGCA	TGCCCACTCCAACAGGTCAAAC

	1309	ATTGGGGAAAACCCGGTCTCAAGG	CCTTGAGACC GGTTTCCCCAAT
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	1311	CGATAGAATTCAATGCAGGGCGGA	TCCGCCCTGCATTGAATTCTATCG
	1312	CGGTCGCTACGGCGGCTGGTTTC	GAAACCAGCCGCCGTAGCGAACCG
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	1317	GATACATGCCGCCTGCTAGGCAC	GTGCCTAGCAGCGGCCGATGTATC
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	1320	CCGAGCTGCACGAGCACACAAAGT	ACTTTGTGTGCTCGTGCAGCTCGG
	1321	TTCCACAAGGCGGCATAGTGAGGC	GCCTCACTATGCCGCCTGTGGAA
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	1324	AGTCACGCCAACGTCGGTTCTT	AAAGAACCGACGTTGGCGTGACT
	1325	AGTGGGCGCACTTGGCCTAAATA	TATTAAGGCCAAGTGCAGCCC ACT
	1326	ACTTGCAACTCGGCCGTTGACT	AGTCAAACGGCCGAAGTTGCAAGT
	1327	CAAACATCAGGTTCATGCCGTACG	CGTACGGCATGAACCTGATGTTG
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	1329	GCAGGCATCCGGCAGAGATGTCTC	GAGACATCTGCCGGATGCCTGC
	1330	GAGCGGCTAACAGAGGCCAGACAAA	TTTGGTCTGGCCTCTAGCCGCTC
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	1332	ACTTGCAAGGCCAACACAAG	CTTGTGTTGGCCTCTGCAAAGT
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	1334	CTACATGCTCACCCCACCAAGAGTG	CACTCTGGTGGGTGAGCATGTAG
	1335	ATTTTCAGAACAGCCCCGCCTCGA	TCGAGGCAGGGCTATTCTGAAAAT
	1336	CAATTGCTACGTTGACGCCCTCTG	CAGAGGGCGTCAACGTAGCAATTG
	1337	CTGTCGCCCTAACCTCGGTGGCG	CGGCCACCGAGGATTAGGCACAG
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	1341	GCTCGCCGCGCGTCTTATGTCTG	CAGACATAAACAGCGCGCGAGC
	1342	ATGAACATCGCGAGGCAAGCCTT	AAAGGCTTGCCTCGCGATGTTCAT
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	1345	GGAGGCATGCCCTCCGAGAGAAC	GTTGCTCTCGGAAGGCATGCCCTC
	1346	CACCGATCCTCAACGCAATTGCTA	TAGCAATTGCGTTGAGGATCGGTG
	1347	GGCCATGAATTGGGAAATCCATGT	ACATGGATTCCCAATTATGCC
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	1368	AGCGTGCCTGGCTATAAGGCTA	TAGCCTTATAGCCAAGCGCACGCT
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	1371	ACTGTGTCGCAATCAACCCGCAA	TTTGCAGGGTTGATTGCGACACAGT
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	1375	CGTACGGACATCGATGACGCAACG	CGTTGCGTCATCGATGTCCGTACG
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	1383	GTATGTGCGGGATGAAATCACGC	GCGTGATTCCATCCGCACATAC
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	1386	ATAAGCGCGCCACAGGTATGTACC	GGTACATACCTGTGGCGCGCTTAT
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	1407	GCGGCTAGTTGACCTAGCGGCTG	CAGCGCTAGGTACAACTAGCCGC
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	1413	GGCAAAGGGTGTATTGGGAGACC	GGTCTCCATAAACACCCCTTGCC
	1414	ACAAGGCTTGGCTGGCAGAAC	GTATTCTGCCAGCCGAAGCCTTGT
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	1417	CCGAACCATGGTTATCCAGTGT	ACACTGGATAAGCCATGGTTCGG
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	1419	GCGCAGTACACCATGATGCTTC	GAAAGCATCATGGTGTCACTGCC
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	1424	GACCTCACGGTCATCAGAGGGAG	CTCCCTCTGATGACCGTGAGGGTC
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	1427	GGTCGGAACGTGTGCGATCC	GGATCGCACAGATCAGTTCCGACC
	1428	TGCTCCTCCTAGGGTCATCCGT	CACGGATGACCCCTAGGAAGGAGCA
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	1441	GGGCCGTAGAGGCATCGGGTAAAG	CTTACCCGATGCCTCTACGGCCC
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	1444	CCCCGATCGGGTGTAAATTCTCCCT	AGGGAGAATTACACCCGATCGGGG
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	1469	ATGCTAGCGCGCCTGTCAACGTAC	GTACGTTGACAGGCGCGCTAGCAT
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1501	CTTCGCAAGGTTCGCAGACAATCC	GGATTGTCTCGAACCTCGAAG
1502	TACGT CCTGTGCTGTTGACACCGG	CCGGTGTCAACAGCACAGGACGT
1503	GTTGGGTCAATGTTGGGGAGA	TCTCCCCGAAACATTGACCCGAAC
1504	CCCTGTTGTAAGGGGTTGTGA	TCACAAAACCCCTTCACAACAGGG
1505	GGCAGATTGGTGAACCCCAGATAA	TTATCTGGGTTCAACATCTGCC
1506	CCCTCGGTGTGTTCAAGCAAATC	GATTGGCTGAACACACCGAGGG
1507	CCCGCGAACATTGAAACAGCTAA	TTAAGCTGTTCAAATGTTCGCGGG
1508	CCGTGTCAGTTGCTCCCTGGCACG	CGTGCCAGGGAGCAACTGACACGG
1509	TCCGTCTCAGCCGCCCTCCATCC	GGATAGGGAGGCGGCTGAGACGGA
1510	ATAGCTGGGTCAACCACAGCGGTC	GACCGCCTGTGGTGAACCAAGCTAT
1511	ATAGGCAAGCGGTGTAGCACAGCG	CGCTGTGCTACACCGCTTGCCTAT
1512	TTAGAACCGGTCTGGATTGCGT	ACGCAAATCCAGACCGGCTTCTAA
1513	TGCCGACCTTACCAAGGATCCTCG	CGAGGATCCTGGTAAAGGTCGGCA

	1514	GCCCCACACTATAACCAAGCTGGCA	TGCCAGCTGGTTATAGTGTGGGC
5	1515	TTGCGCCACTAGTACGGATCTCAA	TTGAGATCCGTACTAGTGGCGCAA
	1516	CTTGCAGTTATGCTGACCCGTCC	GGACGGGTCAGCATAAACTGCAAG
	1517	TGCCTCCAATTACTTACCGCCGT	ACGGCGGTAAAGTAATTGGAGGCA
	1518	CCC GTATGCGGAAGCTATGGGCTA	TAGCCC ATAGCTTCCGCATACGGG
10	1519	TCGTTCAACCCCACACTTCAGTTG	CAACTGAAGTGTGGGGTTGAACGA
	1520	CAATGTGGGGGACATTCAAGGTT	AACCTGAAATGTCCCCACATTG
	1521	TAGCGTCGCACAATGGCTGACCG	CGGT CAGCCATTGTGCGACGCTA
	1522	GGTGGCTTCGTGACAATATCGGCC	GGCCGATATTGT CACGAAGCCACC
15	1523	CAGCGGCGTCCGAAATTGGCTCTC	GAGAGCCAATT CGGACGCCGCTG
	1524	GGCTTGCTCTCGTTTGATTGCA	TGCAATCAAAAACGAGAGCAAGCC
	1525	ATGCGAGGAGGACACGACCGTTCC	GGAACGGTCGTGT CCTCCTCGCAT
	1526	CCTGTTCACTACGACCCACGGAA	TTCCC GTGGGTGCTAGTGAACAGG
20	1527	GTGCCACGGAGTGC GACTGTTGCT	AGCAACAGTCGCACTCCGTGGCAC
	1528	ACACATCCAAGTCTGACGATGGCC	GGCCATCGCAGACTTGGATGTGT
	1529	CAGCCC GAAAGGAAAGCCTCCGTG	CACGGAGGCTTCCCTTCGGGCTG
	1530	AACTGAATGTAGGTGGGCCCTGT	ACAGGGGCCACCTACATT CAGTT
25	1531	ATTTTCGACGATAAGCTGGCCGGT	ACCGGCCAGCTTATCGTCGAAAAT
	1532	TGAGGGAGAACCCGAAATCTGCTT	AAGCAGATT CGGGTTCTCCCTCA
	1533	GGCGACTACATCCCCAATTGCTG	CAAGCAATTGGGGATGTAGTCGCC
	1534	GCAGACGCGGCCTTCCATACTTT	AAAAGTATGGAAGGCCGCGTCTGC
30	1535	ACAACCACATGACGTGTAGCTGCA	TGCAGCTACACGT CATGTGGTTGT
	1536	CTGCTGGGCGCGCAAAGCTTGTG	CAACAAGCTT GCGCGCC CAGCAG
	1537	AAGCCTTCTTGGCTTGCTCCGCT	AGCGGAGCAAGCCAAGAAGGCTT
	1538	TACCTGCTGCCTGGAGCAAGGCAT	ATGCCTT GCTCCAGGCAGCAGGTA
35	1539	GACGCCG CAGCCATGAGTGAGTGT	ACACTCACTCATGGCTGCGCGTC
	1540	AGTTGGCCGCTTATTTGCTACC	GGTGAGCAAAATAAGCGGCCAACT
	1541	CCAGGCGCCTTCGACAGATCCTCA	TGAGGATCTGTCGAAGGCGCCTGG
	1542	GTGTCCCCCTCCAGCTAGCCAGTT	AAACTGGCTAGCTGGAGGGGACAC
40	1543	GACAACAAGCCAAGGTGACACGTC	GACGTGT CACCTT GGCTT GTGTC
	1544	CTACACCGCTCGT GACTCGGCAA	TTGCCGAGTCACGAGCGGTGTAG
	1545	TGGTGCCATCAAAGCACGTTGTAC	GTACAACGTGCTT GATGGCACCA
	1546	ACAATGCGTGTGCGAAACGCATA	TATGCGTT CGCAACACGCATTGT
	1547	TTGTCCAGCCATTGTATTTGCGC	GCGCAA AATACAATGGCTGGACAA
	1548	ACGAGAGATAGCGGACTCCCTCGA	TCGGAGGAGTCCGCTATCTCTCGT
	1549	AGCTTGTGCTCAGGCAGCTTT	AAGAGCTCGCCTGACGACAAAGCT
	1550	GACAGTCGGCGTGCAGTT GTGT	ACAACAAACTGCACGCCGACTGTC
	1551	AGCTAGCGACGGCCAACTCACGTA	TACGTGAGTTGGCCGTCGCTAGCT
	1552	CTCCTGTT CGGGGCCGTTACTGGT	ACCAGTAACGGCCCCAACAGGAG
	1553	ACTGACCGACGCAGTGCACATAG	CTATGTGGCACTGCGTCGGTCAGT
	1554	AGGTAGGGTCTGGTTGACTCGCA	TGCGAGTCAAACCAGACCC TACCT

	1555	CCTCCATTTAGCGCGTTGCCAAT	ATTGGCAACCGCGCTAAAATGGAGG
5	1556	TTCTTAGGATCCGCGCACTCTGG	CCAAGAGTGCAGCGGATCCTAAGAA
	1557	GTCGAAGGTGTCTACCGTGCAG	CTGCGCACGGTAGACACACCTTCGAC
	1558	GTCACTCGCGGCCAATCACTCG	CGAGTGATTGGGCCGCCGAGTGAC
	1559	TCTCGGTACCCGTCTTGACCCCT	AAGGGTCAAGACGGGTGACCGAGA
	1560	GCCCTCGACGAACATCCTGAAC	GTTCAGGATGAGTCAGAGTACGCCGA
	1561	TCCGGCGTACTCTGACACGGCGAT	ATCGCCGTGTCAGAGTACGCCGA
10	1562	AGCCAAATGTTCTGTTGGTCGGA	TCCGAACCACGAAAGCATTTGGCT
	1563	ACTCCACGCCGCATGTTGCTGTGA	TCACAGCAACATGCAGCGTGGAGT
	1564	GCTTCGAGTCGGTGGCATCTGTAT	ATACAGATGCCACCGACTCGAACG
	1565	GGTCTGGGCCATCGACTTGCTGC	GCAGCAAGTCGATGGCCAAGACC
	1566	GGTATCGGACTGCACTAAGGGCAA	TTGCCCTAGTGCAGTCCGATAACC
	1567	AGCCCATGCGTTCCGGATGATTG	CAAATCATCCGGAACGCATGGGCT
	1568	GCCAGGGTTAAAAGTGTATGGGCTC	GAGCCCATCACTTTAACCTGGC
15	1569	GACGACGTGCTGGCTACGAAGGGG	CCCCTCGTAGCCAGCACGTCGTC
	1570	TCCTATTGACCGTGATCGTGTATC	GATCACGATGCACGGTCAATAGGA
	1571	ACCCGCCTCGACTCCACAACAAA	TTAGTTGTGGAGTCGAGGCGGGT
	1572	GATGTGGATCACGACCTGCCAGTA	TACTGGCAGGTGCGATCCACATC
	1573	GTGCCATTGCCACCCATAATGCGT	ACGCATTATGGGTGGCAATGGCAC
20	1574	TTAGCCTGTGCACCCAGTCAGGAG	CTCCTGACTGGGTGCACAGGCTAA
	1575	TCCGATGGGAGAGGCTGATCTCAC	GTGAGATCAGCCTCTCCATCGGA
	1576	CACTACTGAAGTGGCCTGGCGCTG	CAGCGCCAGGCCACTTCAGTAGTG
	1577	TGCGGCCATAGCGATGTGTAGAT	ATCTATCACATCGCTATGGCCGCA
	1578	GATTGCGCTAACGGAGATGCACG	CGTGCATCTCGTTAACCGCAATC
25	1579	TCACGTTGACAACGCCAAGCATT	AATGCTTGGCGTTGTCAAACGTGA
	1580	GCATTGTTGCTAAAGGCGGCATT	AATGCCGCCTTAGCAAACAATGC
	1581	AGTCGCTCTACGCGTGCAACGCTG	CAGCGTTGACGCGTAGAGCGACT
	1582	TAGCTCCATGGAGGTCCGAAAGGG	CCCTTCGGACCTCCATGGAGCTA
	1583	GACCGGTTGGACCTCACTGGCTC	GAAGCCAGTGAGGTCCAACCGGT
30	1584	AAGCCGGACAGTCATGTGCGTAT	ATACGCACATTGACTGTCCGGCTT
	1585	TGCCTCGCTGAGTTCTCACCGTG	CACGGTGAAGAACTCAGCGAGGCA
	1586	TCGTAGACCTGCTTTGGCTCA	TGAGCCCCAAAGCAAGGTCTACGA
	1587	ACCGCTATGCGCCCTACAAAGCAT	ATGTTTGTAGGGCGCATAGCGGT
	1588	TAGCGTCACCGTAGCTGGGCAG	CTGCCCCAAGCTACGGTGACGCTA
35	1589	CTCTCAGCAACTGATGGCACCGGA	TCCGGTGCCATCAGTTGCTGAGAG
	1590	AAAGGAAATGTGGTGCTGGTCGGC	GCCGACCAAGCACCAATTCCCTT
	1591	CCGGCTTAGATGGAGAACAAAGTC	GCACCTGTTCTCCATCTAACGCCG
	1592	AAGTAAATGCCCTGCCAAACCG	CGGTTGGCGAGGGGATTTACTT
	1593	TGGGCTGTTCAAGCCTACCGGACGT	ACGTCCGGTAGGCTGAACAGCCA
40	1594	GTTCGGITCAGCCATGGGCCTAC	GTAGGGCCATGGCTGAACCGAAC
	1595	GGCCAACATTCTAGGGAGTGCC	GGCACTCCCTAGAAATGTTGCC

	1596	TTCCTCGTGGGATTGTCCTCACC	GGTGAGGACAATCCCAACGAAGAA
	1597	TGCACATTGGGTACGGATCTGAC	GTCAGATCCGTACCCAATGTGCA
	1598	GGCAGTTAGACGGCAAATGCAAGG	CCTGCAGTTGCCGCTAATGCC
5	1599	CGCGTCAGGCTATGAATGGCTTT	AAGAGCCATTATGACGCG
	1600	GCTGAATGCAAACCTCGGAGCCAT	ATGGCTCCGAGGTTGCATTAGC
	1601	CGCTCTGGCGGATTCAATTGTTTC	AAAACAATGAATCCGCCAGAGCG
	1602	TTTCAATCAACCCCTCCGGACGTA	TACGTCCGGAGGGTTGATTGAAA
	1603	GTGGTGGAGTCTGAAGCACGACAG	CTGTGTCGTTACAGACTCCACAC
10	1604	AAACAGGTCCGGATGATGTCGGA	TCCAGACATCATCCGGACCTGTT
	1605	GTACCGCGTGTACGCCACCGTTAG	CTAACGGTGGCGTACACCGGTAC
	1606	TCCAACCTACATTGCGGAAGGAA	TTCCCTCCGCAAATGTAGGTTGGA
	1607	GACGTACCGTCGTCCCCTGAGTTG	CAACTCACGGGACGACGGTACGTC
	1608	GGCAATCCTACAACCGACGCTGAT	ATCAGCGTCGGTTGAGGATTGCC
15	1609	GGCGGCTGCAGGGTCTACATCGAG	CTCGATGTAGACCTGCAGCCGCC
	1610	ATACTACGCTGCAGCTGCGCGGGC	GCCCCGCGCAGCTGCAGCGTAGTAT
	1611	GGATCGCAATCCCTCCGATGACGA	TCGTCATCGGAGGGATTGCGATCC
	1612	TGGCCTTGCACGGGAGCCGAATCT	AGATTGGCTCCGTGCAAGGCCA
	1613	AGGTGCCGACGAAACGACGAATAT	ATATTGTCGTTCGTGGCACCT
20	1614	GCTGTTTACCGTCGTCGTTGTTG	CAACAACGACGACGGTAAACAGC
	1615	CGGTCCCAATGTTACAACCCAGAC	GTCTGGTTGTAACATTGGGACCG
	1616	GCAATTCCAGCCACTTTGACCAA	TTGGTCAAAAGTGGCTGGAATTGC
	1617	ACGGGCGAAAGCTCGGTACGGATA	TATCCGTACCGAGCTTCGCCGT
	1618	CGACCCGACTTTGCTTCGAGTG	CACTCGAAAGCAAAAGTCGGGTCG
25	1619	AATTCACTGTTGCGTCATGGTCG	CGACCATGACGCAAACACTGAATT
	1620	CCTGTATGAGGTTCTGGTCGGCT	AGCCGACCCAGAACCTCATACAGG
	1621	TGGCATACTTGGTGCACCGCCGT	ACGGCGTTGCAACCAAGTATGCCA
	1622	TCGCCAGTACAGAAACATGCGGGC	GCCCCGATGTTCTGACTGGCGA
	1623	CCCGCTGTTGCTCTCATCGTGGAG	CTCCACGATGAGAGCAACAGCGGG
30	1624	GCCACAATCTGACCCGGGAATCA	TGATTCCCAGGGTCAGATTGTGGC
	1625	GCTCAGTCTCGGAAGTTCGGCTA	TAGCCGAAACTCCGAGACTGAGC
	1626	CTTCACGGCCAACGACGGTCGAG	CTCGACCGTCGTTGGCCGTGAAG
	1627	CGACAGTCCGTCCTGAGGA	TCCTCAAGACGGACGGAACGTGCG
	1628	ACGGAGACGCACTCGAAACGTCCC	GGGACGTTGCACTGCGTCTCCGT
35	1629	CATGCATCCGATTAAGGGGATCAC	GTGATCCCCTTAATCGGATGCATG
	1630	ATTGCGGGAGTCCCTAGCTTCTG	CAGAAAGCTAGGGACTCCCGCAAT
	1631	GTGTGGAAGATGCAATTGGAACGG	CCGTTCCAATTGCACTTCCACAC
	1632	ATACAACGGTAGGTGACAGGGCG	CGCCCCCTGTCACCTACCGTTGTAT
	1633	GCCGTGGGAGTAAGGGTACAAAGG	CCTTTGTACCCCTACTCCCACGGC
40	1634	GCACGTAGGTGGCTACTACTCGG	CCGAGTAGTAGCCGACCTACGTGC
	1635	ACTGTGATCTTGGGCAAAGGGC	GCCCTTGGCCAAGAGATCACAGT
	1636	CATGCCTGAACAATCTGCATCCC	GGGATGCGAGATTGTCAGGCATG

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1637	GAGCCTGGCTCCACAGCTGTGCTC	GAGCACAGCTGTGGAGGCCAGGCTC
1638	CTTCGATACCATCGTGGCGATC	GATGCCAACGATGGTATCGAAAG
1639	CCCGGAGGTGAGGCATTGAATATG	CATATTCAATGCCTCACCTCCGGG
1640	CTCATTCACTAAAAGCGGCTGGA	TCCAGCCGCTTTAGCTGAATGAG
1641	GAAATGCCCTGGGGACTTTGCC	GGCAAAAAGTCCCAGGGCATTTC
1642	TTTGCCCTCACACAGACGAGCA	TGCTGCGTCTGTTGTGAAGGCAA
1643	AAATCCCAAGACGTGGGGCGTAT	ATACGCCCCGACGTCTGGGATT
1644	CAACGGGCGGTAGCTAAACCGTAA	TTACGGTTAGCTACCGCCCGTT
1645	GGCCAACGACAATGCGAAACCTTC	GAAGGTTCCGATTGCGTGGGCC
1646	GACATCACGCAAAATCTCAGCGCA	TGCGCTGAGATTTGCGTGATGTC
1647	ACGTTCCGTCCACAACCGTATGTT	AACATACGGTTGTGGACGGAACGT
1648	GCTCATAGGTCTCCGTAGCCCGT	ACGGGCTACGGAAGACCTATGAGC
1649	GAAACGAGTCTCTCGCGCCCTAGA	TCTAGGGCGCGAGAGACTCGTTTC
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1651	TGACCGCTCGATACCAGGAGGGTG	CACCCCTCCTGGTATCGAGCGGTCA
1652	CTGGCAATAAAGACCTTCCGACCA	TGGTGGAAAGGTCTTATTGCCAG
1653	TGCGCGACGTATGTTGGTGATTA	TAATCACCAACATGACGTGCGCA
1654	GTTGGTTGTGGGAAACACACCCGCT	AGCGGGTGTGTTCCCACAACCAAC
1655	TGTGGTTCGGAAACACAGGAAGT	ACTTCCTGTGTTCCGAACCCACA
1656	GGAAAAAACGGCAATTAGCCGAGT	ACTCGGCTAATTGCCGTTTTCC
1657	TGGTGCAGGTGCCCTTATTGGG	CCCAATAGAGGGCACTCCGCACCA
1658	AACCAACAGGCTGCAGCCCAGACT	AGTCTGGGCTGCAGCCTGTTGGTT
1659	AAACAGATCCATCTGCACGCCAGG	CCTGGCGTGCAGATGGATCTGTT
1660	GGAATACCGCGGCATTATGGCTT	AAGCCATAATGCCCGGGTATTCC
1661	TACTGTTCGCGCAAACCGTCACT	AGTGACGGTTGCCCGAACAGTA
1662	GATCTCTCGTGGAGCACGTTTCC	GGAAAACGTGCTCCACGAGAGATC
1663	GGCATAGCAAACCTTGACCTCCAA	TTGGAGGTCAAGGTTGCTATGCC
1664	ATCTGGGATTCGCGAGCCAATATC	GATATTGGCTCGGAATCCCAGAT
1665	CGATCAGGATATCATTACGCCCG	CGGGCGTAATGATATCCTGATCG
1666	ACGGTACCGAAACGGCTCAGCGT	ACGCTGAGACCGTTGGTACCGT
1667	CTCCCATACTCGTCTTACCGA	TCGGTAAGAACGCAGGTATGGGAG
1668	GCACGAGAACCTAATTGCGACA	TGTGCGACAATTAGGTCTCGTGC
1669	GCCACACGATCAAGACAGCGCATG	CATGCGCTGTCTGATCGTGTGGC
1670	CCCGTTAACTCACGAGCGGTCAAT	ATTGACCGCTCGTGAGTTAACGGG
1671	AGAGAAGGTCAATTGCGTGTGGT	CACCGACAGGCAATGACCTCTCT
1672	CGGGCCCTTAAAGTAGAGCAGG	CCTGCTCTACTTTAACGGGCCG
1673	ACATCGCGTCCGAGGGAGTAGCG	CGCTAACTCCCTCGGACGCGATGT
1674	AATGCCTAATCGAGCCAGCGGATC	GATCCGCTGGCTCGATTAGGCATT
1675	CTCGATCTTAAACCGGCGCTT	AAGCGCCGGTTAAAAGATCGAG
1676	CGTTCCGTGAAGGCAGGGTCTCAC	GTGAGACCTGCCTCCAGGAACG
1677	CCTGTGCTTACTATCGCGATCCA	TGGATCGCCGATAGTAAGCACAGG

	1678	GTTAGTCGCCATTGGCCTGGTT	AACCAGGCCAATAGGGCGACTAAC
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	1681	TAAGACGCAGAAGATGGGTCCAC	GTGGACCCATCTCTGCGTCTTA
	1682	CACCACAGCTCTTGTTCGACCC	GGGTCGAACAAAGAAGCTGTGGTG
	1683	TCGGGTCCGTACCACCACTTTGC	GCAAAAGTGGTGGTACGGACCGA
	1684	CCAAGCCCCGAGTACCGAAGATT	AAATCTCGGTACTCGGGCTTGG
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	1686	TGTCTGTGTCATGGCACCTCGCAT	ATGCGAGGTGCCATGACACAGACA
	1687	AGGACTGCAGTGTGACCGTCTGAT	ATCAGACGTGCACAGTGCAGTCCT
	1688	CCATCCTCATGTACAGCGCCGCTG	CAGCGCGCTGTACATGAGGATGG
	1689	GTACCCGCGCCTTCCTCGACACAG	CTGTGTCGAGGAAGGCGCGGGTAC
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	1691	CGTATCGAAGGCGTGTACAACCGG	CCGGTTGTACACGCCCTCGATAACG
	1692	TGCCCGCCCTTATGCAACGCTCA	TGAGCGTTGCATAAAGGGCGGGCA
	1693	AAACTTACGAGACGGCGGCTGCCA	TGGCAGCCGCCGTCTGTAAGTTT
	1694	AAGTCTGACAAACGGAACGGGTGT	ACACCCGTTCCGTTGTCAGACTT
	1695	TAAGCGCAGACCAAAGTATGCGGC	GCCGCATACTTGGTCTGCGCTTA
20	1696	GCAGTTTTCAGATCCTCCGCAAA	TTTGCAGGAGGATCTGAAAAACTGC
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	1698	CACAGAAACGGTTAACGAAACGCC	GGCGTTCGTTCAACCGTTCTGTG
	1699	GCATGCTCAGATGGTCGTGCTCAC	GTGAGCACGACCATCTGAGCATGC
	1700	AAGGATTCTCGCTCCGGCATGAT	ATCATGCCGAAGCGAGAACCTT
25	1701	GGTGGGGTAGCGCTGGTATGAAAA	TTTCATACCAAGCGCTACCCCACC
	1702	ATTATTACGGGACCGAACCAACGG	CCGTTGGTTCGGTCCCGTAATAAT
	1703	GCGCGAGTGTCATGATGTTACGT	ACGTGAACATCATGACACTCGCGC
	1704	GACATTCTGACTTGGTCGTCCGC	GCGGACGACCAAGTCACGAATGTC
	1705	TCATTAGTCGAGGCACCGATCAAG	CTTGATCGGTGCCTGCACTAATGA
	1706	GAGTTGTGCCGAGTCATCGGAGTC	GACTCCGATGACTCCGCACAACTC
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	1708	ATGGCGTTGCGAACGTCATACAG	CTGTATCGACTTCGCAAACGCCAT
	1709	TGCATCGGCCCTAACAGAGAACT	AGTTCTCTGATTGAGGCCGATGCA
	1710	ACAATCATGGCAATCTGGCAAATG	CATTTGCCAGATTGCCATGATTGT
	1711	GACGTGGAAGAGTGCAGATCAGCA	TGCTGATCTGCACTCTCCACGTC
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	1713	GCATAGGGCGAATCTAGTACGGC	GCCCGTACTAGATTGCCCTATGC
	1714	TCCGGCGCATCCTCATTAGCAACT	AGTTGCTAATGAGGATGCGCCGG
	1715	TGGCCGCTTCACTAATATTGGAC	GTCCAATATTAGTGGAAAGCGGCCA
	1716	CCGGCGGACGGCTTGTCAATGA	TCATTGACAAGAGCCGTCCGCCGG
40	1717	CGAGCAACCCAAAAGGAAGCAGTA	TACTGCTTCTTTGGGTTGCTCG
	1718	GCGTATGATTGGCAATCCGCCAG	CTGGCGGATTGCCGAATCAGC

	1719	AGTACCGCTACAACGCTGGTCGC	GCGAACCCAGCGTTAGCGGTACT
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5	1721	CCACTTCTGTGACCGAACCGTGC	AGCACGGTTCGGTACAGAAGTGG
	1722	CCTGGTACCAGGCAGCAGTTGATT	AATCAACTGCTGCCTGGTACCAAGG
	1723	TAGGGTACCGTCGAGAGACGCCA	TGGCGTCTCTGACGGTACCCCAA
	1724	GGTTGCTTGTGCGCGTGAGGTAGT	ACTACCTCACGCGCACAAGCAACC
	1725	TGCTTCGACCGATGAAACTCGAAG	CTTCGAGTTCATCGGTCGAAGCA
	1726	TGCCACCCATACTATGCCAGTGG	CCACTGGGCATAGTATGGGTGGCA
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	1728	TGAGAGAAAGCTGGCTCGGATCAG	CTGATCCGAGGCCAGCTTCTCTCA
	1729	TATTGCGAATTGAGTACGTGCC	GGGCACGTACTCGAATTGCAATA
	1730	CGAGAGGGTTCCCAGTGATCGA	TCGATCACTGGGAACCCCTCTCG
	1731	TGCCTGGGTGTCGTTCAATTCT	AGAATTAGAACGACACCCCCAGGCA
15	1732	GTGCGTCATTGTGGTCATCCAA	TTGGGATGACCCACAATGACGCAC
	1733	AGGGCTCCCAGCATACCAACGTTG	CAACGTTGGTATGCTGGAGCCCT
	1734	AACTAGCCGCACCTTGTGCAGAG	CTCTGCACAAAGGTGCGGCTAGTT
	1735	TTAGCCCAGCCCTCAATGGGAAC	GTTCCCATTGAAGGGCTGGCTAA
	1736	CGGCCTCGGTTGACGGGTAGTCT	AGACTACCCGTACAACCGAGGCCG
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	1738	GATGGTTCGCCCTTGTGCGCAGC	GCTGCGACACAAGGGCGAACCATC
	1739	GAGATTCAATACAGGCCGCGGTC	GACCCGCGGCCTGTATTGAATCTC
	1740	AGGGCGAAGGAAGGTTCCGTTTT	AAAAACGGAACCTTCCTCGCCCT
	1741	CTCGACCCCTGCCACTACTGGTTC	GAACCAGTAGTGGCAGGGTCGAG
25	1742	TGTTCCCGGGTCTACGCATTACTG	CAGTAATGCGTAGACCGCGGAACA
	1743	GAGACGACGTCCCTACACCCGCTAA	TTAGCGGGTGTAGGACGTCGCTC
	1744	AGATTGCGACAGCGACACGTGATT	ATACACGTGTCGCTGCGAATCT
	1745	GATACCGTTGGCATTCTCGGTA	TACCGAGAAATGCCAACGGTATC
	1746	GATTGGGAGGCATTAGCGACCGGA	TCCGTCGCTGAATGCCCTCCAATC
30	1747	AGGAGGAAACGAGGGCGTAGGTT	GAACCTACGCCCTCGTTCCCT
	1748	GCCAAACAACGTCTGACGCCCTAGC	GCTAGGCGTCAGACGTTGGC
	1749	TTAACGCGAAAGGATGCACCGCG	CGCGTGCATCCTTCGCATTAAC
	1750	TTATCGGCCGTTAAATGGGATGG	CCATCCCATTAAACGGCCGATAA
	1751	CCTGGATTGTTACCGCTAGCA	TGCTAGCGATGAACGAATCCAAGG
35	1752	AAGTGAACGTGCAGTGGCTTCGA	TCGAAGACCACTGCACGTTCACTT
	1753	TCCTTACCCCTCGTCAACGCC	AGGCCTTGAACGAGGGGTAAGGA
	1754	ATTCTGAACCATGCATGCCCTGT	ACAGGCCATGCATGGTTAGGAAT
	1755	AGCGAGACGCTCGATCACGAACTA	TAGTCGTGATCGAGCGTCGCT
	1756	GCTGGTCTGGCTCGTGTAGAA	TTCTAACAGCGAGCCAGACCAAGC
40	1757	CGTGCAGGGCATAAAGATAGGTCT	AGACCTATCTTATGCCGCGCACG
	1758	TCTGGCACTCACATCGGACAGTCT	AGACTGTCCGATGTGAGTGCAGA
	1759	ACCATTGGAGGACCACAGAGCTCC	GGAGCTCTGGTCCCTCAAATGGT

	1760	TCCAGGGTCGGAGTACATGGCGGG	CCCGCCATGTACTCCGACCCCTGGA
5	1761	ATATGCCGTGCGATCGTACACGCA	TGCGTGTACGATCCGACGGCATAT
	1762	TGCTGGCGTCAACACTCCCGATT	AATCGGGAAGTGTGACGCCAGCA
	1763	CAGGGCGGTGCGGTGAACTAGCCA	TGGCTAGTTCACCGCACC GCCCTG
	1764	CATGGACTGCCGTACATCAGCTGG	CCAGCTGATGTACGGCAGTCCATG
10	1765	CCGGCCATACGCTGGCAAGATTAC	GTAATCTGCCAGCGTATGCCCGG
	1766	AGCGGACACCTGTACTCTCCCA	TGGAGGAGAGTACAGGTGTCCGCT
	1767	GGAGCCACACCAGTCGAAGATGGT	ACCATCTCGACTGGGTGGCTCC
	1768	CGCCACCGGAAATTGAAAAGACTG	CAGTCTTTCAATTCCGGTGGCG
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	1770	TTGAAGCGGTGAAGAGCCTGTCCT	AGGACAGGCTCTCACCGCTTCAA
	1771	CGAACCAAGCTGCATTGTCAGTGG	CCACTGACAATGCAGCTGGTTCG
	1772	GAGTCTGCGCTTGCAATCTTGCG	CGCAAAGATTGCAAGCGCAGACTC
	1773	GCTGGGTATAGTTGCCCTGGCAATG	CATTGCCAGGCAACTATAACCCAGC
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	1775	GCGCCAACTAATACCTCCACCGCG	CGCGGTGGAGGTATTAGTTGGCGC
	1776	TGGCGTTCA GTGCAACGCTGGTTA	TAACCAGCGTTGCACTGAACGCCA
	1777	CAAAACTGACGGGTATGGGAGCGC	GCGCTCCCATACCGTCAGTTTG
	1778	AGGTGTCGCTGGAACCCGACTTGT	ACAAGTCGGTTCAGCGACACCT
25	1779	CTTCCAAAAGCGCAATTGGCTTTG	CAAAGCCAATTGCGCTTTGGAAG
	1780	TCGGGCTTCTCGCAATTCTGTCA	CTGACAGAATTGCGAGAACCCGA
	1781	GCCAAAAGAATGCGCTGGTAGGT	ACCTACCCAGCGCATTCTTTGGC
	1782	TGGTGC CCGCACCGAGAGACTGTA	TACAGTCTCTCGGTGCGGGCACCA
	1783	CGAGGCCGTAGTGGGACTGCTCT	AGAGCAGTCCCCACTACGGCCTCG
30	1784	CGATCTGCGCATAGAGGGGACTTT	AAAGTCCCCTCTATGCGCAGATCG
	1785	TGTGCAATGGCCTTCTCAGAGCC	GGCTCTGAGAAGGCCGATTGAC
	1786	GATCACCTGGACCGCTACCGTTT	AAAACGGTAGCGGTCCAGGTGATC
	1787	ATGGGGAGTTAAGGACCCCTGCACC	GGTGCAGGGCTCTAACCTCCCAT
	1788	CATTGTGGACAGCCAATGGTGGCT	AGCCACCATTGGCTGTCCACAATG
35	1789	CCATCACCATGCCACGGTAAGATC	GATCTTACCGTGGCATGGTATGG
	1790	GCACCCGTGTCGTTGGTAGCAAG	CTTGCTAACCAACGACACGGGTGC
	1791	GGAGTGGTTCCCGGAATTCACTG	CAGTGAATTGCGGAACCCACTCC
	1792	GGGGATTTCTTCGCAAGGCTCGA	TCGAGCCTGCGAAAGGAAATCCCC
	1793	CATTGATCATGTGCACTGCACCA	TGGTGCAAGTGCACATGATCAATG
40	1794	AGCAGCGCTGCGCTTTCGAT	ATCCGAAACAAGCGCAGCGCTGCT
	1795	CGAGTAACGCCGGTTGCTTGC	TTCGCAAAGCAACCGCGTTACTCG
	1796	TGGCCTGGAACATAGGTGGAAC	GAGTTCCACCTATGTTCCAGGCCA
	1797	CGCACACCAAGCGTTATTGAGAA	TTCTCAATAACGCTGGTGTGCG
	1798	TCACCTTCACAGTGGCATA CAGC	GCTGTATGCCACTGTGAAGGTGA
	1799	CAAATATCCCTGAGCCCTCGAGCT	AGCTCGAGGGCTCAGGGATATTG
	1800	GGGAGCTGGTGAGCAGATGTAACG	CGTTACATCTGCTACCAGCTCCC

	1801	AGGATTGCTTTGCCTTATGCGGA	TCCGCATAACGCAAAGCAATCCT
5	1802	ATCGTTGGCGCTACGCAATTGT	ACAATTGCGTAGCGCCAAACGAT
	1803	CCGATTGTCCCAAATGCAACGTT	AACGTTGCATTGGACAAATCGG
	1804	AAGGGTCAAGCTCATGGAGCGGAA	TTCCGCTCCATGAGCTTGACCCCT
	1805	TCTGACGTCGTTCAAGGGCTCGCT	AGCGAGCCCTTGAACGACGTCAGA
	1806	CGCACCACTCCGAGGTATTGTCT	AGACAAATACCTCGGAGTGGTGCG
	1807	AAGGGTAAAAAGGAGAACCGGA	TCGGCTTCTCCTTTCACCCCCTT
10	1808	AAACCACGCAAATGGCGATACCAT	ATGGTATGCCATTGCGTGGTT
	1809	CAGAAGGGATGACGCCCTAACGTCG	CGACTTAAGGCGTCATCCCTTCTG
	1810	CATGACGAGAGCGGACCTGAAGTG	CACTTCAGGTCCGCTCGTCATG
	1811	CTGGACATGTTGTTGCCACTG	CAGTGGCGAAACAAACATGTCCAG
	1812	AAGACCGACTCTCGTCGTTGCAC	GTGCAAACGACGAGAGTCGGCTT
	1813	GCGCGATTACATACCGTTCCGTA	TACGGAAACGGTATGTAATCGCGC
15	1814	CACTGACCGGACCCAACCTAACAT	ATGTTAGGTTGGTCCGGTCAGTG
	1815	AGTGCAAGTCTAGACACGCCCGAG	CTCGGGCGTGTCTAGACTTGCAC
	1816	GGTTGGTGCAGATCCTGGACTGT	ACAGTCCAGGATCTGCACCAACC
	1817	GGTCGTCCCGAAACGTAACGAGG	CCTCGTTACGTTGGGACGACC
	1818	GACTAGTACGATCACGGGGCGGGT	ACCCGCCCGTGATCGTACTAGTC
20	1819	CCGACCTGACCCCTGTGTACAGGTT	AACCTGTACACAGGGTCAGGTCGG
	1820	TGCTCACTGCCAACACTGTTATGG	CCATAACAGTGTGGGCAGTGAGCA
	1821	CGAGGAAACACATTCCTCGGGCC	GGCCCAGAAAATGTGTTCCCTCG
	1822	TGGCACCGGGTGGATTCTGTCTA	TAGACAAGAATCCACCCGGTGCCA
	1823	GAGGCACGGTGATAGTGGTTGTG	GCACAACCACTATCACCGTGCCTC
25	1824	ATGCAGATGGATCTTTCGACGC	GCGTCGAAAAGATCCATCTGCAT
	1825	TGCGATAGCCAAAGAGTCGAGGAC	GTCCTCGACTCTTGCTATCGCA
	1826	ATGGCGTGTCAAGCAGTCGCTGG	CCAGGCAGTCGCTGACACGCCAT
	1827	CAATGCAGCTCGGAAGTCAGGTCG	CGACCTGACTTCCGAGCTGCATTG
	1828	AGGATCAGTGCACATGTCCCCCTCA	TGAGGGGACATGTGCACTGATCCT
30	1829	CACATCTGGCTGTACCCGAGAA	TTCTCGGGTGACAGCCAAGATGTG
	1830	CGCATTATCACCTCAATGCCAGTG	CACTGGCATTGAGGTGATAATGCG
	1831	ACATCCGCAAGACTCCCTATAGCCC	GGGCTATAGGGAGTCTGGGATGT
	1832	GTGAACCCGAACGAGGGGAGTC	GAGACTCCCTCGTTGGGTTCAC
	1833	GCGTAGGGAATTGCCTACGACT	AGTCGTAGGCAAATCCCTACGC
35	1834	TTTACGCGTCGCTCGTTGTAGTG	CACTACAACCGAGCGACCGTAAA
	1835	GAGAGGCGTCTAGGCGGTTAGC	GCTAGAACCGCCTAGACGCCCTCTC
	1836	GCATGCTGATAACGAATGCTCCC	GGGAAGCATTGTTATCAGCATGC
	1837	CTGAAGCTCGTGTGCGATGAGGG	TCCCTCATCGCACACGAGCTTCAG
	1838	ACAACGGCATGAGGAGGCTTTTC	AAAAAAGCCTCTCATGCCGTGT
40	1839	TTTGGAGACGCCAGTACGCGTGGT	ACCACGCGTACTGGCGTCTCCAAA
	1840	GCTATCATTGGTGTAAAGCCGCC	GGCGGGCTTACACCAAATGATAGC
	1841	TCAACATCCAGGGCGGTGCTTGGT	ACCAAGCACCAGCCCTGGATGTTGA

	1842	TTCGATGTAATCCCCAAAGATGCC	GGCATCTTGGGGATTACATCGAA
5	1843	GGACCTTCGGCAGGTTATGCCGT	ACGGCGATAACCTGCCGAAGGTCC
	1844	AGTAAGAAGAGGCAGGCCACCT	AGGTGGGCCTGCCCTTCTTACT
	1845	AACGGCTCCCCGTGACTGCTTA	TAAGCAGTACGACGGGAGCCGTT
	1846	CCTATACCGTCGTGGTCCACGTT	AACGTGGAACCACGACGGTATAGG
	1847	CCGCGCAGGCGCTAATACTCAAGG	CCTTGAGTATTAGGCCCTGCGCGG
	1848	AAATGGGCCAGTGAATCCTGGT	ACCAAGGATTTCACTGGCCCATT
10	1849	ACGGTTTCAAACTGCTGGCAG	CTGCCAGCAGTATTGAAACCGT
	1850	CCGCTTGAGGTTCAAGGTAGAGCT	AGCTCTGACCTGAACCTCAAGCGG
	1851	ATCGTGCCCGAAGACACTTAAACG	CGTTAAGTGTCTTGGGCACGAT
	1852	ACCTGAACCAGGGCATTGCTTA	TAAAGCAATGCCCTGGTTCAAGGT
	1853	ACCCTATACGCTGGCTAACGGG	CCCGCTTAGCCCAGCGTATAGGT
	1854	TGTTTCGCGACTAGAACGTTTC	GCAAAGGCTTCTAGTCGCGAAACA
15	1855	GAAGTTGGCGGCTCACCGTATTA	TAATACGGGTGAGCCGCCAACTTC
	1856	TGGCTACACCGCTTAGGAGGAACC	GGTTCCCTCTAACGGGTAGCCA
	1857	CCACAGTTGCGTGACTTACATCGC	GCGATGTAAGTCACGCAACTGTGG
	1858	ACTGCCACTGCGCTGAAGAGTGG	CCACTCTTCAGACGCAGTGGCAGT
	1859	GCGCCAGCAAATTCTGTGTTGT	ACACCACACGAAATTGCTGGCGC
20	1860	TGCCTCCGTCGAGCCGAATAGCCA	TGGCTATTGGCTCGACGGAGGCA
	1861	GTACAAACGGCGCTATTCGTC	GGACGAAATAGGCCCGTTGTAC
	1862	GCTTCCCTGGCTCTGAACGGAAAC	GTTCGTTCAAGGCCAGGGAAAGC
	1863	CGGCTACCCAGGCAGATAAGCTGA	TCAGCTTATCTGCCCTGGGTAGCCG
	1864	GGTTGGACCCGACAGGGAATTCC	GGAAATTCCCTGTCGGGTCCAACC
25	1865	GGGGAATACCGCGCTTGTAAATA	TATTACAAACGCCGGTATTCCCC
	1866	TGGTTCGGTGAGGTTATGTTGGT	ACCGAACATAACCTCACCGAACCA
	1867	TCGGTAGGGTTAGTCGCTGAGGA	TCCTCAGCAGTGAACCCCTACCGA
	1868	TTCGGAGTGTGCCGGTAGTAC	GTACTAGCACCGGACACTCCGAA
	1869	TCGTACTGGAATGATGGCCGGGCC	GGCCCGGCCATATTCCAGTACGA
30	1870	TCCGTCGACCGTCCACCGAACGTT	AAACTCCGCTGGACGGTCACGGA
	1871	AGGGAAATATAACAACACCGCGCAC	GTGCGCGGTGTTGTTATATTCCCT
	1872	ATGTCCCAGGAAACCGAGTACCTCA	TGAGGTAGCTGGTTCCGGGACAT
	1873	ACCAGCGACTTAGATAGCCGTCG	CGGACGGCTATCTAAGTCGCTGGT
	1874	GGAAAACCTCCTTGCCTAACCA	TGGTTGACGCAAAGGAGGTTTCC
35	1875	ACGTGCGTGCATACCAAGAGGAC	GTCCTCTGGGTATGCACGCACGT
	1876	ACGCCACTTCCCTAGAACCAACG	CGTTGGTTAGGGAAAGTGGCGT
	1877	CGAAGTACGCAATAGGCCACCT	AGGGTGGCACTATTGCGTACTTCG
	1878	GATCCCGGGGATCACCTATCAAT	ATTGATAGGTGATCCGCCGGGATC
	1879	AGAAAGCGACCGTTCAAGCTAGC	GCTAGCCTGAAACGGTCGTTCT
40	1880	CGCTCCCTTCATAGTCCTCTCG	CGGAGAGGACTATGAAAGGGAGCG
	1881	GTGGGTGGTCATAACGACAGCAGA	TCTGCTGTCGTTATGACCACCCAC
	1882	CTGGAGGCTGCATCGTTGTAACA	TGTTACGAACGATGCAGCCTCCAG

5	1883	CACCATGAGTTTCGGAGCGAGGAT	ATCCCTCGCTCCGAAACTCATGGTG
	1884	CAAGCTCGTTCGATGAGAGATTG	CAATCTCTCATCGAACGCAGCTTG
	1885	CCTGGGAGCAATGACCGCTCTGGT	ACCAGAGCGGTATTGCTCCAGG
	1886	TCCGGCGCTCTACCAAGATGAGAC	GTCTCATCTGGTAGAGCGCCGGA
	1887	CGACCGCGTCGCGTATACTATCCG	CGGATAGTATA CGC GAC GCG GT CG
	1888	AACATT CG CTAG TGGGGTCCAACA	TGTTGGACCCC ACTAGCGAATGTT
	1889	TGTATGATCATCCGACCGAGCAGC	GCTGCTCGGT CGG ATGATCATA CA
	1890	AGTGC GCC GAG AGGGTGAATAGAC	GTCTATT CAC CCTCTCGGCGCACT
	1891	AGGCTTGTCTGGACCA CG ACCAT	ATGGTGTGGTCCAGAAC AAGCCT
	1892	GGGGCCACATAAAGAATTCCGAAAC	GTTCGGAATTCTTATGTGGCCCC
	1893	TGGTGAAGATAAAATCCGATGGCA	TGCCATGCGGATTATCTTCACCA
	1894	ATTCCACCA CG CT TGG CCAAAT	ATTGGCAAGAGCGTGGTGGAAAT
	1895	CGCGTAAAGCTGTCACCGATGACC	GGTCATCGGTGACAGCTTACGCG
	1896	TCCCCAACCGGTAAACAACAGCGAC	GTCGCTGTGTTACCGGTTGGGA
	1897	CCTCTGCTCGCCTTACACCCATGG	CCATGGGTGTAAGGCGAGCAGAGG
	1898	CAAGCTGCTCCTGTGCTGAAGGGC	GCCCTTCAGCACAGGAGCAGCTTG
	1899	AAACGAACGATGGTCGGTAGACCG	CGGTCTACCGACC ATCGTTCGTT
	1900	TCAGTTCGATGGCTATTGCGCTC	GAGGCGCAATAGCCATCGA ACTGA
	1901	GGCTCTAACGGACGCAAATCATA	TATGATTGCGTCCGTTGAGAGCC
	1902	AGTAGAGTGTGCGGCTGCCGATC	GATCGGCAGCCGCAACACTCTACT
	1903	AGACACTAGACCGCCGTGACCTGA	TCAGGTACGGCGGTCTAGTGTCT
	1904	ACCGAGCACCGAATTCTTGTCC	GGACAAGGAAATT CGGTGCTCGGT
	1905	CCGTGGCCAAGATA CGAACGAATT	AATT CGTT CGTATCTGGCCACGG
	1906	CCTCCTACAGCATCCACATGAGGG	CCCTCATGTGGATGCTGTAGGAGG
	1907	CACTCGGCAAATACGTATGCGCAT	ATGCGCATA CGTATTGCGAGTG
	1908	ACCGAGTTGAAGCACGAATTGGG	CCCAAATT CGT GCTTCAACTCGGT
	1909	GACCACCTCGGAAGATCGTCTGC	GCAGAACGATCTCCGAGGTGGTC
	1910	TCAA CTGGCAAACCGAAGAGCACA	TGTGCTCTCGTTGCCAGTTGA
	1911	GCTTAGCCTCACACGTGCATACCA	TGGTATGCACGTGTGAGGCTAAC
	1912	CTCGGTCTCCAAGTACCAATTG	CGAAATGGTACTGGAGACCGCAG
	1913	GTTCCGTATTACGGCGGCCATAAG	CTTATGGCCGCCGTAAACGGAAC
	1914	ATCGACGCAACCGGATAGTCTCTG	CAGAGACTATCCGGTTGCGT CGAT
	1915	CGCAGATAAACCGGCATCTTCAG	CTGAAAGATGCCGGTTATCTGCG
	1916	ACCTGCCAATACGGGTCTACGGTT	AACCGTAGACCCGTATTGGCAGGT
	1917	ACACCTGTTGCCATGCTGATCCGT	ACGGATCAGCATGGCAACAGGTGT
	1918	AAACTGTCTACTGCGCAATTCCGC	GCGGAATTGCGCAGTAGACAGTTT
	1919	GCAACTAGCCCGTGTAGGATCGT	ACGATCCTAGCACGGGCTAGTTGC
	1920	TCGTAGTGGTGGATTGTTGCGT	ACGCACAACAATCCACCACTACGA
	1921	GGCTTACTCCTCAATTGCGACACG	CGTGTGCAATTGAGGGAGTAAGCC
	1922	CACGACTCCCTGCCAGATTGATT	AATCAAATCTGGCAGGGAGTCGTG
	1923	CTTAGACGTCGGCAATGTCACGTC	GACGTGACATTGCCGACGTCTAAG

5	1924	CTCAGAGCACAAATCTGCCCTGCCT	AGGCAGGGCAGATTGTGCTCTGAG
	1925	GCTAGGAAAGTCGGCATTCAATGGG	CCCATGAATGCCGACTTCCCTAGC
	1926	AAAGCCCCAAAATTCCGCCTAAC	GGTTAGGCGGAATTTGGGCTTT
	1927	GCGCAACGCTAAGGGACTATCAAG	CTTGATAGTCCCTAGCGTTCGCG
	1928	CGTCCGCTGGGATGAGTCTCCTGC	GCAGGAGACTCATCCCAGCGGACG
10	1929	ACAGGCCTCGTATTGGTGTGGGT	ACCCACACCAATCAGGAGGCCTGT
	1930	CATTCTCCTCCGGGACCACGCCT	AGGCGTGGTCCCAGGAGGAGAATG
	1931	TCGGAGTTGACCAAGCTCAGTGC	CGCACTGAGCTTGGTCAACTCCGA
	1932	ACCGGCCACTGCAATTGAAACAC	GTGTTGCAATTGCAGTGGCGCGT
	1933	AGTTCATGGAGCCGGTATTGTT	AACAATACGCCGGCTCCATGAAC
	1934	ACGTTAATGCGGGGCCCGCCTAC	GTAGGCGGGCCCCGCATTAAACGT
	1935	TGAGGCTTAGCCTACGCGCAGGT	ACCTGCGCGTAGGCTAAAGCCTCA
	1936	CAGCGTTATGAGCGCGGAGTTAT	ATAAAACTCCCGCCTACAAACGCTG
	1937	GTCCACGTGACCACGGATAGTTGG	CCAACATCCGTGGTCACGTGGAC
15	1938	GATTATGCTCCTACGCCCTGCTCCG	CGGAGCAGCGTAGGAGCATAATC
	1939	TCGTCAAGGGCATGATGTGTGGG	TCCCCACACATCATGCCCTTGACGA
	1940	GATGGACCGCCAAGAACACCTTGA	TCAAGGTGTCTTGGCGGTCCATC
	1941	TACACGAGGATGGGGTCAAGCTT	AAAGCTTGACCCATCCTCGTGT
	1942	ACACGCACAAAACGTTGAAAGGC	GCCTTCAAACGTTTGCGTGT
20	1943	GTTATCGTGGGCCATGGTACTGA	TCAGTACCATCGGCCACGATAAC
	1944	ACATGACCGTATCCGCCTGCTCG	CGAAGCAGCGGATAACGGTATGT
	1945	GAAGGCAGAACCACTGAAACTACGC	GCGTAGTTCACTGGTTCGCCCTC
	1946	TGACTTTGCAACGGGTGGAACCA	TGGTCCACCCGTTGCAAAAGTCA
	1947	TGAATTCTAGGTTGGTGC	CCGCACCCAAAACCTACGAATTCA
25	1948	AGCATTATGAAGCGGCCATTGCG	CGCAATGGCCGTTCATAAATGCT
	1949	TGCTCCTCGCGTTGGTACCGTGAG	CTCACGGTACCAACCGGAGGAGCA
	1950	CGCAGCAAGAACAGCAACTGTTG	CAACAGTTGCTGTTCTGCTGCG
	1951	AGACGCTGGAGTAAAACCGGA	TCCGAGTTTCACTCCAAGCGTCT
	1952	CATTCTAGAATGCCCAAATGGA	TCCATTGGGGCATTCTACGAATG
30	1953	CCAGAAGGTTGGGACCGCTGTG	CACGACGGGTCCCACCTCTGG
	1954	GAGAAGCCGGTTCTCAGAGCACAT	ATGTGCTCTGAGAACCGGCTCTC
	1955	TTGCGTTGCAAGATATCTGGCCCG	CGGGCCAGATATCTGCAACGCAA
	1956	GGGTTGCATGTTCAAGGCAAGACGA	TCGTCTTGCCTGAACATGCAACCC
	1957	CTCACGAAGGTGACATATCACGCC	GGCGTGATATGTCACCTCGTGT
35	1958	GCCCCGAGATACGGGTTCAAAAAGA	TCTTTGAACCGTATCTGGGC
	1959	CATCTCGCGCTTCTCACTCCGC	GCAGGAGTGAAGAACCGCGAAGATG
	1960	TTACACGGTAAGCGTACGGCCGCC	GGCGGCCGTACGCTTACCGTGTAA
	1961	ACCTTCGGACAATGTGGCGTTCG	GCAGAACGCCACATTGTCGAAGGT
	1962	TGAATGGTTCTGCTAGGCCACAC	GTGTGGGCCTAGCAGAACATTCA
40	1963	CACGCCCTGTCTGACATATGGATGC	GCATCCATATGTCAGACAGCGTG
	1964	CGCCTCAACCCAAATCTGAGAACGT	ACGTTCTAGATTGGGTTGAGGCG

	1965	TTACGCTTACTGCGAGCTGGGTCC	GGACCCAGCTCGCAGTAAGCGTAA
	1966	GGCTTGTGGGGCAATACGCATCTT	AAGATGCGTATTGCCCAACAGCC
5	1967	CACTCTCCTTGGATGCGGAACAA	TTGTTCCGCATCCAAGGAGAGTG
	1968	GACCAGCCATCACGTAACGGCCCT	AGGGCCGTTACGTATGGCTGGTC
	1969	AGGAACCGGATGTGGTTATGGAGC	GCTCCATAACCACATCCGGTTCC
	1970	ATCCATGGGCAACTGAGCCTATGC	GCATAGGCTCAGTTGCCCATGGAT
	1971	GGAACAGCACTTGTACCGCCCCAC	GTGGGCGGTAACAAGTGCTGTTCC
10	1972	TGGCTCGCTTCAAGCCTGTTGCT	AGCAAACAGGCTTGAAGCGAGCCA
	1973	CAAACGTGAGGTCATGACCACCAT	ATGGTGGTCATGACCTCACGTTG
	1974	ACCGATGTCTTGAAGTCCGGAGGT	ACCTCCGGACTTCAAGACATCGGT
	1975	CGAAAATGCATGATGATCTCCCCT	AGGGGAGATCATCATGCATTTCG
15	1976	TTTGGTATTCTCGCTGCACCGTTG	CAACGGTGCAGCGAGAATACCAAA
	1977	GCGTACTCAACCACATTCCCACC	GGTCGGGAATGTGGTTGAGTACGC
	1978	AGCAAACAAACAGCGGTCCGAGCAT	ATGCTCGGACCGCTGTTGTTGCT
	1979	GGACTAGGAGCGGGGATAGCTGAG	CTCAGCTATCCCCGCTCCTAGTCC
	1980	CCTTAACGAAAACCTGTCGACCGC	GCGGTCGACAGGTTTCGTTAAGG
20	1981	CTCGATCGCATAAGCAAGAAACCG	CGGTTCTGCTTATGCGATCGAG
	1982	CCCGTTGTTGGCGACAAAAAGT	ACTTTTGTCGCCAACAACGGG
	1983	CGGCGGCTCTCGCATGATCTCGTT	AACGAGATCATGCGAGAGCCGCCG
	1984	CGGATGGAGAGGAGTCTACGTCCC	GGGACGTAGACTCCTCTCCATCCG
	1985	CAGAACAAATATCGTGCCTAACCG	CGGTTGACGCACGATATTGTTCTG
25	1986	CCTTGCGCGCTCCGAGTAAGGTA	TACCTTACTCGGAGCGCGCAAAGG
	1987	GGAAACGGCACCTATCTGCGTGA	TCACGACAGATAGGTGCCGTTCC
	1988	CGACCGACAAAACCAATGCCGCC	GGCGGCATTGGTTTGTGGTCG
	1989	CCAAGGGTGTGGAGCTGAAGAGA	TCTCTCAGCTCCCACACCCCTGG
	1990	TTAAGTGCCTAGTCCTCGTGGG	CCCACGAGGACTATGCGCACTAA
30	1991	GCCTGGTGGGTAAGTCATGATGC	GCATCATGACTACCCACCGAGC
	1992	GAGCAGCAGATTGATGCGCTTATG	CATAAGCGCATCAATCTGCTGCTC
	1993	TGCGCCAACCTCCGGAATATTGC	GCAAATATTCCGGAAGTTGGCGCA
	1994	AACCCCACATGAAATGCTCTCCG	CGGAGAGCATTTCATGATGGGTT
	1995	GTCCAACGGTACTGGCGTATGTT	AACATCACGCCAGTACCGTTGGAC
35	1996	ACTCGGCTGATCGTGAGATGGTGA	TCACCATCTCACGATCAGCCGAGT
	1997	ATTCGTGGCGCATCTCGGAATGT	ACATTCCGAGATGCGCCCACGAAT
	1998	TCCCGTCCTGTAATCCAGGGAAACA	TGTTCCCTGGATTACAGGACGGGA
	1999	CTTCGCTGCACCTACATTGCGCCA	TGGCGCAATGTAGGTGCAGCGAAG
40	2000	GCGTGTAGATGACTGTGCTTGGG	CCCAAAGCACAGTCATCTACACGC
	2001	CTATGGTATCGAGACATCGGCGGA	TCCGCCGATGTCTCGATACCATAG
	2002	CCTCGTACTCCGTCGTATGCACAA	TTGTGCATACGACGGAGTACGAGG
	2003	TGGTGCCTCCGTAGTGCCTGCACT	AGTGCAGGCACTACGGACGCACCA
	2004	CGCGATCCTAGTTGAAAGCTTGC	GCAAAGCTTCAACTAGGATCGCG
	2005	ACGATCCAGGTGTTGGGACTAAG	CTTAGTGCCCAACACCTGGATCGT

	2006	CCAATCTAGGATACACCAACGCCG	CGGGCGTGGTGTATCCTAGATTGG
	2007	GATACGTGGGTATAGCGGGCCC	GGGCCCCGCCTATACCCACGTATC
	2008	CATGGAACAAACCGTCGTAGGGGA	TCCCCCTACGACGGTTGTTCCATG
5	2009	ACACTCGCCAGTATCGAGTCGT	ACGACTCGAATACTGCGCAGTGT
	2010	CTCAGTCTCGAAGGTGATCCGACC	GGTCGGATCACCTCGAGACTGAG
	2011	TCCCAATCCCCGTGGTATCGTCGT	ACGACGATAACCACGGGATTGGGA
	2012	AATCAACGTAGTCCGGTGGTCCG	CGGACCAACCGGAACCTACGTTGATT
10	2013	CTTAACAACCCAGGGTTGGGCT	AGCCCAAACCCCTGGGTTGTTAAG
	2014	CTACCGCTGCATGGCGTTAGATTG	CAATCTAACGCCATGCAGCGGTAG
	2015	TTATTGGTGGCGGACGGAGTGAGT	ACTCACTCCGTCGCCACCAATAA
	2016	TTAAGGTGAACTCACCGCGTGA	TCACGCGGTTGAGTTCACCCCTAA
	2017	TTTGATTGAAACGCTGCGCACTAC	GTAGTGCAGCGTTCATCAATCAA
15	2018	TCATGTGTAGGTGCGGGCGTCAC	GTGACGGCCGCGACCTACACATGA
	2019	CTCCGAACCTCTGGGCCTCTTT	AAAAGAGGCCAGAAGGTTGGAG
	2020	CTGTTGCCATTGGCCCGACACTC	GAGTGTGGGCCAATGGGCAACAG
	2021	CACGATCGCTGAGCAACACATCAC	GTGATGTGTTGCTCAGCGATCGT
	2022	CGGATCATAAGCGTCCGCCCTCGT	ACGAAGGCCGACGCTTATGATCCG
	2023	AGGTTAACGCAACATGTGATCCGC	GCGGATCACATGTTGCGTTAACCT
20	2024	GGGAAAAACAGCTAACGCTTGCAGA	TCGCAAGGCTTAGCTGTTTCCC
	2025	ACTTATTGCCGGGATCCGTACACA	TGTGTACGGATCCGGCAATAAGT
	2026	TGCGGTCTGGAAAGGAAGGGAGGG	CCCTCCCTCCCTTCCAGACCGCA
	2027	GCTGCCACCTGGACATCGCATACA	TGTATGCGATGTCAGGTGGCAGC
	2028	GCAGGCATGACAGTGGCGTAGTAC	GTACTACGCCACTGTATGCCCTGC
25	2029	GC GGCCCTGATGGTTGGCTGAGC	GCTCAGCCAAACCATCAGGCCGC
	2030	TCCCCATTAGTCCCTCCATCAC	GTGATGGAGGGACTAAATGGGGA
	2031	GCAACACAAATGCGAGCGTAGGAG	CTCCTACGCTCGCATTGTGTTGC
	2032	GGCGTTGTATTGAGCCACGTAG	CTACGTGGCTCGAATACAAACGCC
	2033	GGTAACGTCGCACGTGGAATTCCG	CGGAATTCCACGTGCGACGTTACC
30	2034	ACTTCACAAACGCTCCGTTGGACAC	GTGTCCAACGGAGCGTTGTGAAGT
	2035	CCGAATTATAAGCGCAAGGCACA	TGTGCCCTGCGCTTATAATTGG
	2036	GGACCCGATAAGACTCTGACGCCG	CGGCGTCAGAGTCTTATCGGGTCC
	2037	ACCCGTTCTCGTAGGAACCTGCT	AGCAGGTTCTACGAGAAACGGGT
	2038	CACGTTCACTGTATCTGGTTGCC	GGCAACCAGATACTGCGAACGTG
	2039	CCTCGGATGGGCCATGACCTTGA	TCAAGGTATGGGCCATCCGAGG
35	2040	GGACGCCCTGCTGTAGGGTTTGAT	ATCAAACCCCTACAGCAGGCCGTCC
	2041	CTCGAGCGTGGCTAAAGAGCAT	ATGCTTTAGCCCACGCTCGAG
	2042	TTTACTTCTTAGGGCGCGTTGGG	CCCAAACGCCCTAAGAAGTAAA
	2043	ACCACCAACATAGCGCGCACTAGT	ACTAGTGCAGCGCTATGTTGGTGGT
	2044	TGGTTACACGGCAGCCCGCGTAAG	CTTACGCGGGCTGCCGTGTAACCA
40	2045	TTATGGTACGTTGCTGCGTGCAGG	CCCGCACGCCAGAACGTACCATAA
	2046	ACCGCGGATCTAACGAATCCCATT	AATGGGATTGTTAGATCCCGCGGT

	2047	CATGATCCGCCCTAGGTTAAC	GCTTAACCTAAGGGCGGGATCATG
5	2048	TACCGCTTCAAAGGGTGCGAA	ATTCCGGCAACCCTTGAAGCGGT
	2049	GCACCGCGTCAATATTACCGAGG	TCCTCGGTAATATTGACGCGGTG
	2050	GTGTCGCGGTTACAGAAGGAGA	TCTCCTTCTGTAAGCCGCGACAC
	2051	GCAAGCCATACCGCAATAACTG	CGAGTTATTGCGGTATGGCTTG
	2052	ATGAGGTGCGTGCCTACAGAG	CTCGTGAACGCAGCACGACCTCAT
	2053	CGAGACTAGTGCGATGCAGGGT	TACCCCTGCATCGGCACTAGTCTG
10	2054	GCCTCATCATAGACGCTGGATG	TGCATCCAGCGTCTATGATGAGG
	2055	GACAGGCGTCGGAAGCTCTCAAG	CTTGAGAGCTTACCGACGCCGTG
	2056	GCTACGAATCTTCCCTGTCGCCAC	GTGGCGACAGGGAAAGATTGCTAG
	2057	TTTGGCAGAACGTACCAAGGGGT	ACCCCACGGTACGTTCTGCCAAA
	2058	GGACAATAAGCACCGGAGATGCG	CGCATTCTCCGGTGCTTATTGTC
	2059	TCATGAACCTTCTGATGCCGCGA	TTCGCGGCATCAGAAGGTTCATGA
	2060	CGCCGCATTACCTAAAAACGTG	GCACGTTTTAAGGTAATGCGGCG
15	2061	ACGAGTCCAACCGCCATTGATT	AATCAATGAGGCAGGTTGGACTCG
	2062	GCGAAGAGTTGCTACTCTTCCGCC	GGCGGAAGAGTAGCAACTCTTCG
	2063	CGTCGGCAACAATCTTTCGTGA	TCACGAAAAAGATTGTTGCCGACG
	2064	AATCCTGTGCACCGTGAGACCG	CGCGTCTCACGGGTGCACAGGATT
	2065	AACCTATATGCATCACGCGAGCC	GGCTCGCGTTGATGCATATAGGTT
20	2066	GAACCTGGCAAAACAGCCCGAAA	TTTCCGGGCTGTTTGCCAAGTTC
	2067	CTCTATGGCGTTGCCGTCTGCA	TGCAGACGGCAAACGGCCATAGAG
	2068	AGTGCACCGGGTTGTTGACACAAT	ATTGTGTCACACCCGGTGCAC
	2069	CCTGGCTTTACACGCCAAGAAA	TTTCTGGCGTGTGAAAAGCCAGG
	2070	CACTCAGCGTAGCCTGAAGCCTGG	CCAGGCTTCAGGCTACGCTGAGTG
25	2071	GAATTATCGACCGCAGCGGTGCG	CGACACCGCTGCCGTGATAATT
	2072	GTGACATCACATGGTGGCCAGCG	CGCTCGGCCACCATGTGATGTCAC
	2073	AGCACCTGCCAGTCACCAAGTGA	TCACTGGTACTCGGAAGGTGCT
	2074	TAGGTTGCAGGAATGGTGGCACC	GGTCCCACCAATTCTGCAACCTA
	2075	GTCCCATACTGTGGTACCGGAT	ATCCCGTACCAACACGTATGGGAC
30	2076	TCGGATACTCTCGCGTGCACGGG	CCCGTGGCACGCGAGAGTATCCGA
	2077	CAACGTTGCCCTAAGCCCAAAT	ATTGGGCTTAGGGCGAACGTTG
	2078	GTTAGGTACCCGGCATATCTTA	TAGGATATGCCCGGGTGACCTAAC
	2079	GTTACCCGGCTCTACTGGGTT	AAACCCAAGTAGAGGCCGGTGAAC
	2080	AATCCCGCTAGGTATGTGGTC	GACCACATGACCTAGACGCGGATT
35	2081	GCTACGCCCTGGAGGTGGTACCC	GGGTACCACTCCAGAGCGTAGC
	2082	CAGGGAAATGCTACAAAGGGTCAA	TTGGACCCCTTGTAGCATCCCTG
	2083	AAGGGTTAGCTGCCCGGTTAACAG	CTGTTAACCGGGCAGCTAACCTT
	2084	CCTCGCAAGCGCGATATTATGCC	GGCATAAAATATCGCGCTGCGAGG
	2085	GCCTCCCGGTATGGTCAAGGGAA	TTCCCTTGACCATGACCGGGAGGC
40	2086	GCTGTTGAGCGGGCACCTGTGCA	GTGCACAGGTGCGCCGCTAACACAGC
	2087	CGCTGACTTAGCTGTGCG	CGGCACATCAGAGCTAAGTCAGCG

	2088	TTCATGGCATTCATCACGAAGGAA	TTCCCTCGTGTGAATGCCATGAA
5	2089	TAGTGTTATGCCCGCGTGTGAATG	CATTACACCGCGGGATAACACTA
	2090	CATGTAAGGGCACGGCGTGGCA	TGCCCACGACCGTGCCTTACATG
	2091	CAGGAAGCTCGCTCCGTGTGAC	GTGCATCACGGAGCGAGCTTCTG
	2092	CCTGCTGATAGCAACCTCACTGCA	TGCAGTGAGGTTGCTATCAGCAGG
	2093	ACTACGAGGGCAGGGCTAGGCG	CGCCTAGACCCCTGCCCTCGTAGT
	2094	CATAATGTGGGTGCTGACGCCGAT	ATCGGCCTCAGCACCCACATTATG
10	2095	TAGCGAACACACAGAGCCGCTC	GAGCGGCTCTGTGTGGATTGCTA
	2096	TCGCGAAATCCCTAAATCCTGTGC	GCACAGGATTAGGGATTTCGCGA
	2097	TGGCACGAATCAAGCCACCAACTC	GAGTTGGTGGCTTGATCGTGCCA
	2098	GCGGACCGCTTTGCTATCTGACG	CGTCAGATAGCAAAGACGGTCCGC
	2099	AGGCCCCGCCCTGTAAATTGGTCAT	ATGACCAATTACAAGGCGGGGCCT
15	2100	CTGGTCCCATAACGCCGCTGACTAG	CTAGTCAGCGCGTATGGGACCAG
	2101	TGCTAACTCGGCCCTACAGAGTC	GACTCTGTAGGGCCGCAGTTAGCA
	2102	TGGTTTATGTCGGTAGCGTCCG	CGGACGCTACCGAACATAAAACCA
	2103	AGCTAAACCTCTCCACGGGATG	CATCCCGTGGGAGAAGTTGAGCT
	2104	CGCGAAGATAGTGAATCCGCATC	GATGCGGATTTCACTATCTCGCG
	2105	GAGTGAACACCTCTCGCGGGTTGCA	TGCAACCCCGAGAGGGTTCACTC
20	2106	TCGAATGCTCTGCAGTGACGTCAA	TTGACGTCACTGCAGAGCATTGCA
	2107	AGGTGGCAATGATCGACGACCTG	CAGGGTCGTCGATCATTGCCACCT
	2108	GTCCGGAGGCCGTGCAAAGCAATAA	TTATTGCTTGCACGGCTCCGGAC
	2109	CTTTGGGATTAGAGGCCGACAA	TTGTCGGCCTTAATCCCCAAAAG
	2110	GGCATAAAGGCTTCCGTTCTGTC	GACAGGAACGGAAGCCTTATGCC
25	2111	GCGGACCGTAAAGCGGGCAGATAG	CTATCTGCCGCTTACGGTCCGC
	2112	TTTCAAGAGTCATCGAATCCACG	CGTGGATTGCACTCTTGAAA
	2113	CCGGCATCCCTCTCGCTTGGCC	GGCAACAGCGAGAAGGGATGCCGG
	2114	ACACAGAGACCGAACGGAGTGCA	TGCACTCCGTTCGCGTCTGTGT
	2115	AGCGGCATTCTCCACTCGTTACT	AGTAACGAGTGGGAGAATGCCGCT
	2116	GGAGCGTACTCGCCCTCGCAAGTC	GACTTGCAGGCGCAGTACGCTCC
30	2117	AAACCGAATGACACGGCAGATAA	TTATCTGCCGTGTCAATTGGGTTT
	2118	AACCAAGCGGATCGATAAAACGACA	TGTCGTTTATCGATCCGCTGGTT
	2119	GGTGTCCACCCGTTAACGCCGGA	TACCGGCGTTAACGGGTGGACACC
	2120	AGCGCGACGTGGCTTGGCTAAA	TTAACGGCAAGCCACGTCGCGCT
	2121	TCCCACGGCTATAGGTCCAACGAC	GTCGTTGGACCTATAGCCGTGGGA
35	2122	ATCAACGAAACGATGCCGTAGGTG	CACCTAACGGCATCGTTCGTTGAT
	2123	GAGGCTAAGCCGTATGGCCGAGGC	GCCTCGGCCATACGGCTTAGCCTC
	2124	ACGGTCCGAAATGGTTAGAGGCAC	GTGCCTCTAACCAATTGGACCGT
	2125	ACGCAAACCATCCCTCGAGTAGGC	GCCTACTCGAGGAATGGTTGCGT
	2126	TTACACGCTCGCTATTGGGCCATA	TATGGCCCAATAGCGAGCGTGTAA
40	2127	CTCGGCACGGGTTAGAACGCCGG	CCGGCGTTCTAAACCCGTGCCGAG
	2128	ATTCGGTAAGGTATCGGGCTAGCG	CGCTAGCCGATACCTTACCGAAT

2129	AGCACACCGTTATACATGACGGCG	CGCCGTATGTATAACGGTGTGCT
2130	AGTCCCTGCCGTCGCTCATGGAA	TTCCATGAGCGAACGGCAGGGACT
2131	GGGCTTATGACCAGTCAGGTTGGA	TCCAACCTGACTGGTCATAAGCCC
2132	GGTCACCACACGAGTCGCTGGTCT	AGACCAGGCACTCGTGTGGTGACC
5	TTGATCGTGTCTCCGAAACCTCT	GAGGGTTTCGGGAGACACGATCAA
2133	ATTGTGCGATCGGCATTTCTAA	TTAAGAAATGCCGATCGCACAAT
2134	GGGTCCAACGACTTCGCTGCTG	CAGCAGCGAGAAGTCGTTGGACCC
2135	CAAATTCCCTGGGGGCCATAGTGG	CCACTATGCCCCCCAAGGAATTG
2136	CCAGAGTATCCGCCGTAGACGGT	ACCGTCTAACGGCGGATACTCTGG
10	TCCTGCAGATCATCTCGTGTCTGG	CCAGACACGAGATGATCTGCAGGA
2138	TGCGGGAGATTGAAACAAGCTGTA	TACAGCTTGTCAAATCTCCGCA
2139	TTAGACGCCGAGCTAGGCAACGTC	GACGTTGCCTAGCTCGCGTCTAA
2140	TTTCGGCAGAATCTCCGATTCAAC	GTTGAATCGGAGATTCTGCCGAAA
2141	TGGCGAGCAGACCTACAAGACAGA	TCTGTCTTAGGTCTGCTGCCA
15	GGCGACAGACCGGTACATCGGCCA	TGGCCGATGTACCGGTCTGCGCC
2143	TCTAGACCTGCGTTCTGGGGACC	GGTCCCACGAAACGCAGGTCTAGA
2144	GCCGAGCGTGGTACCATACGTTCA	TGAACGTATGGTACCAACGCTCGGC
2145	TAATCACACCCGCTTCTGTGGCT	AGCCACAGAAAGCGGGTGTGATTA
2146	GGCCGGAGCCATTGGACACTTCTT	AAGAAGTGTCCAATGGCTCCGCC
20	CCTGTAGACCTGCATGGATCGTG	CAGCGATCCATGCAGGTCTACAGG
2148	ATCGCCGTCCCCGCAAAATAAGCA	TGCTTATTTGCGGAAACGGCGAT
2149	TGGATCAACGGGGTAGTGAAAACG	CGTTTCACTACCCCGTTGATCCA
2150	AAGCGACGATGCTTCTTGAGCTG	CAGCTCAAGAAAGCATCGTCGCTT
2151	CACGGGCACGTGTTACGCTTG	GCAAGCGTAGAACACGTGCCGTG
25	ACGGGCTGGACAAGAGCTAGAAA	TTTCTAGCTCTGTCCCAGCCCGT
2153	GGTAACTGGCTCCGCTCTCACATC	GATGTGAGAGCGGAGGCCAGTTACC
2154	ACTCTGGCTGTTGGCGAACGTGAC	GTCACGTTGCCAACAGCCAGAGT
2155	GACCGAGGACCAGTCCTGCTCTC	GAGAGCAAGGACTGGTCTCGGCC
2156	AGTAGCTCTGGCCCTAACGGCA	TGCCGTAGGCCAAGAGCTACT
30	TTCTTGTCTGGGGAGAGCAGTG	CACTGCTCTCCCCCAGGACAAGAA
2158	TTAGCAGGGAGGTTGTCGGCTCAT	ATGAGCCGACAACCTCCCTGCTAA
2159	AGAACGTGGATTGTACGCTCCGCC	GGCGGGAGCGTACAATCCACGTTCT
2160	CTTCACAGCCTGGAGCCACCAATG	CATTGGTGGCTCCAGGCTGTGAAG
2161	GAGATCGATGAAACGCACCAGCGG	CCGCTGGTGCCTTACGATCTC
35	GGGTCCAGAGTTGGTGGATAA	TTATCCCACACCAACTCTGGACCC
2163	CCGTCCACCCCAGATAGGAATCAC	GTGATTCTATCTGGGGTGGACGG
2164	TGCCTCGCTCTGTGAATCTACGA	TCGTAGATTACAGAAGCGAGGCA
2165	GATCACAGCGTCCGCGCATAACGG	CCGTTATGCGCGGACGCTGTGATC
2166	ATGACGCCCTACATGACGCACCTT	AAGGTGCGTCATGTAAGGCCTCAT
40	GGGTGGAATAACGCCCTAGTTCA	TGAACTAAGGGCGTTATTCCACGC
2168	GGTCTACCATTCTGCCCGACCG	CGGTGGCGAGAAATGGTAGACC
2169		

	2170	ACACCTCTCTGGCGTAGACGCTCA	TGAGCGTCTACGCCAGAGAGGTGT
5	2171	GTAAGAGGTGCTCAGGACTCGTCGC	GCGACGAGTCCTGAGCACCTCTAC
	2172	GTAAGCAGGAGGCGAAGGCGCGAA	TTCGCGCCTTCGCCTCTGCTTAC
	2173	TCTAAGGGCCGTTCAATCGACCT	AGGTCGATTGAAACGGCCCTAGA
	2174	AACCTGATTTCAGGGTCAGCCCGA	TCGGGCTGACCCCTGAAATCAGGTT
	2175	GTCACGCGATTGGCCCACCTATTA	TAATAGGTGGCCAATCGCGTGAC
	2176	ACGATGCCCGCATGTAACCTAGT	ACTAGGTTACATGCGGGCATCGT
10	2177	TGAGAGATGTCTCGTCAACGCCCTG	CAGGGCTTGACGAGACATCTCTCA
	2178	GCATATCTCGCGGTGACAGACGAA	TTCGTCTGTCACCGCGAGATATGC
	2179	GACCCAACGTCGAAATTGTGCGAT	ATCGCACAATTTCGACGTTGGGTC
	2180	TGAAAATCGGGGCATCTAGTTGG	CCAAACTAGATGCCCGATTTCA
	2181	CCCGGAAAAGGATTGTGTACCGA	TGGTACACAAATCCCTTCGCGG
	2182	CATTCCATTATCCGAGTCGCT	AGCGAACTGCGGATAATGGAATG
	2183	CCTGTCTGTCGAGCCAGCGTCTAT	ATAGACGCTGGCTCGACAGACAGG
15	2184	TCAGCGCGCTAACAAAGTTATGC	GCATAACTGTTAGCCGCGCTGA
	2185	ACGCCTACGAACGACCCAAGAGAG	CTCTCTGGGTCGTCGTAAGCGT
	2186	TGCGCATCTACCATTGTGTGGATC	GATCCACACAATGGTAGATGCGCA
	2187	AAGTCCCGCGCTCGCTCCTGTAATA	TATTACAGGAGCGAGCGCGGACTT
	2188	GCTGGGTATTGCTCGAGTAACCA	TGGTTACTCGAGCAATGACCCAGC
20	2189	TGGAGCGTTCTGCAATGACCGAC	GTCGGTCATTGCCAGAACGCTCCA
	2190	CAAGTCAAATTCTGGCAATTCCG	CCGAATTGCCAAGAATTGACTTG
	2191	CGTTCATGCAAGGATCCCAGGTTA	TAACCTGGATCCTGCATGAACG
	2192	ATGCCAATAGAAGCTGGGGATGCT	AGCATCCCCAGTTCTATTGGCAT
	2193	CCTAACTCTCCCTGAGGCCGTT	GAACGGCCTCAAGGGAGAGTTAGG
25	2194	ATCTCGCGAAGGTTCAAACATT	AATGTTGGAACCTTCGCCGAGAT
	2195	GCGACAGATTACGCTCGGTTTC	AAAAACCGCAGCGTAATCTGCGC
	2196	AAGCCCAGACGCCAACACGTTAC	GTAACGTGTTGCCGCTGGCTT
	2197	TCAAGTTCAAATCACATCCCGTGG	CCACGGGATGTGATTGAACCTGA
	2198	GATTGTCGTTCTGTCGTGAGGCG	CGCCTCACAGACAGAACGACAATC
30	2199	ACCGAACTATGTCGGCATGGCA	TGCCATGCCGAACATAGTCGGT
	2200	CGTCATGGGTGTGCAATGCCGTT	AACGGCATTGCACACCCGATGACG
	2201	CGGACGGAGTCACGTTGTGCACT	AGTGCACAAACGTGACTCCGTCG
	2202	TAAACAAGTCGTGTGCCCTTGCCG	CGGCAAAGGCACACGACTTGTGTTA
	2203	TAATTACTGGCTGTGGAGCAGGC	GCCTGCTCACAGGCCAGTAATTA
35	2204	GGAGCGGCCGAATGGTGCTCTTA	TAAGAGCACCATCGGGCCGCTCC
	2205	ACTAAGCAAGGCTGGATGTGCGT	ACGCACATCCAAGCCTGCTTAGT
	2206	GGCAGCTCAGCGGCAGTACGCTAC	GTAGCGTACTGCCGCTGAGCTGCC
	2207	GCGAGGCCAATTATCCGCGGATT	AAATCCGCGGATAATTGCCCTCGC
	2208	CATACGACACACCTGGGGTGCTA	TAGCACCCCAAGGTGTGCGTATG
40	2209	TGCTTGGGCTTTAAACCCCGTTT	AAAACGGGGTTAAAGCCCAAGCA
	2210	CCGGTTGGAAAACGCAAATATCGG	CCGATATTGCGTTCCAACCGG

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2211	AAACTAGCTAGCCGCACCCGCAAG	CTTGCGGGTGCGGCTAGCTAGTTT
2212	GTTGTTCCACCAAGTATCACGCCAG	CTGCGTATCACTGGTGGAAACAAC
2213	GCCGCTGACAAGATGATCATCGTT	AACGATGATCATCTGTAGCGGC
2214	CTTCATAAAGCCAACCGATGCC	GGGCATCGGTTGGCTTATGAAAG
2215	CTGACTGCATCTGAAAGCGGGTG	CACCCGTTTCGAGATGCAGTCAG
2216	ATTCTTCGGAGAACCGGCCACGT	ACGTGGCCGATTCTCCGAAGAAAT
2217	CATTTGGGCCCTAGCTACTGCGC	GCGCAGTAGCTAGGGCCCAGAAATG
2218	CCGATCCCGCACATCCGTATCTG	CAGGATACGGATGTGCGGGATCGG
2219	TATCACCGGGAGCGTCTTATCGT	CACGATAAGACGCTCCGGTGATA
2220	TAGGGCTCGTGCACCGATTAGAGG	CCTCTAATCGGTGCACGAGCCCTA
2221	GCGTGGCACTCGCTTGTCTAGGT	TACCTAGACAAGCGAGTGCCACGC
2222	CTCAACGAACTCAAGGGCCGCTAC	GTAGCGGCCCTTGAGTTGTTGAG
2223	AGCCTGGTATCGACCAATCCTGCA	TGCAGGATTGGTCGATACCAGGCT
2224	TACCGGTTCTAGTTGCCGGATCC	GGATCCGGCCAAGAACCGCTA
2225	TTTATGGGTTGTGCCTGATGGGT	ACCCATCAGGCACAAACCCATAAA
2226	GGGACCCCTAGCAACGTCACCTTA	TAAGGTGACGTTGCTAGGGTCCC
2227	CTGCCTCCCCAGGAGTCATTGGAT	ATCCAATGACTCCTGGGGAGGCAG
2228	AACCCCGCAAGACCAGTACCAATC	GATTGGTACTGGTCTTGCAGGGTT
2229	GGTCACATA CGCGCTAAAAGCGC	GCGCTTTTAGCGCGTATGTGACC
2230	AAATGGCTCCGACCAGTTAGGAC	GTCCCTAACTGGTCGGAGCCATT
2231	AACCGGGACGCTAAAGGTGCAT	ATGCACCTTAAGCGTGCCTCGTT
2232	GATCGCACGCCGATTAACCTTACA	TGTAAGGTTAACCGCGTGCATC
2233	CCTCCTGATTGGGAGTGCAGGATT	AATTCCGCACTCCAAATCAGGAGG
2234	CGGAGGGTAATAGGCTCTCTGCG	CGCAGAGGAGCCTATTACCTCCG
2235	ACAAGAACTGGACATTACCGCGGG	CCCGCGGTAATGTCCAGTTCTGT
2236	TGTCGTCTAAAGGCCTTGTGCG	CGCACAAAGGCCTTAAGACGACA
2237	GGTGACCATGTGGCTTTAGCTT	AAGCTAAAAGCCACATGGTCACC
2238	CACGGTTGCGCACGGTACCAAGAAC	GTTCGGTACCGTGCAGGCAACCGTG
2239	CCTTATTGTTGGCTCCCTGCC	GGGCAGGGGACCAAAACAATAAGG
2240	GTGCGCCTGCATTCTACCGTCAAT	ATTGACGGTAGAATGCAGGCGCAC
2241	GTTCACGTTGATGGCTTGCCTCG	CGGCGGCAAGCCATCAACGTAAAC
2242	CCGTCGGTGGTAGGACGTGAATGT	ACATTACGTCCTACCAACCGACGG
2243	TGATCGCCCCAGAATCCCTGTGCT	AGCACAGGGATTCTGGGGCGATCA
2244	AAGCAGCCAAAAATCGGTTGCTT	AAAGCAACCGATTTGGCTGCTT
2245	CGACGGGACTTAGTAGCAGGGCCT	AGGCCCTGCTACTAAGTCCCCTCG
2246	CCGATTGCGAACGACCAAGTAG	CTACTTGGTCGTTCGCGAATCGG
2247	CCACCCCAACTCCAATCTTCTCA	TGAGAAAGATTGGAGTTGGGGTGG
2248	GTGCAGTAGACGACTACCGCGTC	GACGCCGGTAGTCGTACTGCAC
2249	TTCGCCCATCGTATCAAGCAATT	GAATTGCTTGATACGATGGCGAA
2250	GAATGCGACTACCGCTGGGTCA	TGACCCGACGGGTAGTCGCGATT
2251	CCAGCACTGCCATCGGTTATAAT	ATTATAACCGATGGCGAGTGCTGG

	2252	CGAACCGTAGAACTCCGGTCGGT	CACCGACCGGAGTTCTACGGTTGC
5	2253	GCACCATGACAGAGCCCCAGGATG	CATCCTGGGCTCTGTATGGTGC
	2254	TGGGCTACCGCAGAATAAGGGTGA	TCACCCATTATTCTGCGGTAGCCA
	2255	TGGCCTGTCGTGCGAAGGAAACA	TGTTTCTTCGACACGACAGGCCA
	2256	GCCTCACCGATAGCGAGCGTTGC	GCAAACGCTCGCTATCGGTGAGGC
	2257	GTGCGCGCCGGCTAAAACGAGACA	TGTCTCGTTTAGCCGGCGCGCAC
10	2258	CCGCAGACGAGTTCTTGACAG	CTGTCACAAGAAACTCGTCTGCGG
	2259	GTTCGCAATCGCGTAGGAAGC	GCTTCCTAGCACCGGATTGCGAAC
	2260	TGTTGTACACATGCATCCGGTGA	TTCACCGGATGCATGTGTACAACA
	2261	CACTGAACACGATATAAGGGCG	CGCGCCCTTATATCGTGTTCAGTG
	2262	CGCGATGGTCTTAGCAAGACGAT	ATCGTCTGCTAAGAACCATCGCG
	2263	TACACCAAGGAAGAAATGGGACG	CGTCCCCATTCTTCTTGGTGT
15	2264	CGTGCCTTGCCTTGGTGCAGC	GCTGCACCTAAAACGCAAGGCACG
	2265	GTCGTTGTCTGGCATTACGGC	GCCGTTAATGCCAGACAAACGAC
	2266	CAGGCTCTGTTGGTACAAACGT	ACGTTGTACCGAACGGAGAGCCTG
	2267	CGGACACTGTTCACCAAGACCA	TGGGTTCTGGTAAACAGTGTCCG
	2268	TACCCATGATGCGGAAGAACGTA	TACGCTTCTCCGCATCATGGT
	2269	CTGTCCCTAACCGGGATGAGAACCG	CGGTTCTCATCCGCTAACCGACAG
20	2270	CGGGAGATGAGAACGGTTGTGC	GCACAAAACCGTTCTCATCTCCG
	2271	TAGATCGCAGCTGTACTCAGGCCG	CGGCCTGAGTACAGTCGCGATCTA
	2272	AAAAACAGTTCGCGCACTGTCGT	ACGACAGTCGCGCGAAGTGT
	2273	CGAGGAGCTCCACATAAGCCCAAT	ATTGGGCTTATGTGGAGCTCCTCG
	2274	TGGCTAGGGATGGGAATCATCTT	AAGATGATCCCCATCCCTAGCCA
25	2275	AGGATTGGTGCCCTGGATGCATTG	CAATGCATCCAGGCACCCAACTCCT
	2276	TGTATCTACCGGCCTGAAGCAGGT	ACCTGCTTCAGGCCGGTAGATACA
	2277	TCCCTACGCGCATGACTCGCTTAC	GTAAGCGAGTCATGCGCGTAGGGA
	2278	TGGTCGATCACCTGTGACAGACGC	GCGTCTGTCACAGGTGATCGACCA
	2279	TGGGGGTAGTCCATGCATCAATTG	CAATTGATGCATGGACTACCCCCA
30	2280	CCCTGCCAGGATTACTATTCCGGA	TCCGGAATAGTAATCCTGGCAGGG
	2281	TCCCGCACGGGAATTAAAGTAGA	TCTACTAAATTCCCGTGCAGGG
	2282	GTGATGTGCAGGAACCTCTGTCGC	GCGACAGAAGTCCCTGCACATCAC
	2283	ATTAGGCATGCATGCGCTTCTCA	TGAGAAGCGCATGCATGCCTAAAT
	2284	TTCGGCGCTAGTGGACGCCGTCAA	TTGACGGCGTCCACTAGCGCCGAA
35	2285	GAGCTTCATCTCATCAGTCCGCG	CGCGGAAC TGATGAGATGAAGCTC
	2286	GACAACTCCACTGCTCCAATCGCA	TGCGATTGGAGCAGTGGAGTTGTC
	2287	GGCCAAGGATGGACCTTACGATGG	CCATCGTAAGGTCCATCCTGGCC
	2288	GGTTCGGAATTGTCACCGCTTC	GAAGCGGTGACAAATTCCGGAACC
	2289	GCGCTGGATAGTCTGCGAGAACCC	GGCTTCTCGCAGACTATCCAGCGC
40	2290	TGAGTCCAGTGCTGCCACCATGAA	TTCATGGTGGCAGCACTGGACTCA
	2291	TTGAATTGGGTGTGGAGCGTTCT	AGAACGCTCCGACACCCAAATTCAA
	2292	CGGCGGGCAGACAATGCTTGAAC	GTTCAAAGCATTGCTGCCGCCG

2293	GGGTCTGTCAAAGAGGGTGTCTGG	CCAGACACCCCTTTGACAGACCC
2294	CTTGTGCAAGACGAAGCACCCTT	AAGGGTCTCGTCTGCACAAAG
2295	ATCGAATTCCGAGGAGGTCTCCAT	ATGGAGACCTCCTCGGAATTGAT
2296	TCCGACCCCTCAGAGTCGACTCATT	AATGAGTCGACTCTGAGGGTGGGA
2297	ATCAACGGCACCTCCTCGCCGAG	CTCGCGAGGAGGTGCCGTTGAT
2298	AGCCACGGAATAATTCCGTCACC	GGTGGACGGAATTATCCGTGGCT
2299	GATCGCTTGGTATCGCAAAGACT	AGTCTTGGGATACGCAAGCGATC
2300	TCCACGCCCTACCATCAACTGCAA	TTGCAGTTGATGGTAAGGCGTGG
2301	GCCAAGCGATAGGCCAGAACTCAG	CTGAGTTCTGGCTATCGCTTGGC
2302	AGCGTGTGGGTCACTTACGACGA	TCGTGCTAAAATGACCCACACGCT
2303	GTTATGCGCGGCTTACGAGTTCGA	TCGAACTCGTAAGCCGCGCATAAC
2304	TCTGTCCACGTAACTTGCCTGCAG	CTGCAGGCAAGTTACGTGGACAGA
2305	TCGGCAGCCAATGATCATACCTCT	AGAGGTATGATCATTGGCTGCCGA
2306	TAAGCCCAGTCCGGTCCGTGTTT	AAACACAGGACCGGATCGGGCTTA
2307	ACATGGCAGACTAACAGGCCCTCGC	GCGAGGCCTGTTAGTCTGCCATGT
2308	CATGGCTGCACTCTAACGTCGACG	CGTTGACTTAGAGTGCAGCCATG
2309	TCTTCACCCACGCGGAACGATTG	CAATCGTCCGCGTGGGTTGAAGA
2310	CTCGTGTCTCCAGAGGATTGTCCTC	GGGACAATCTCTGGAGACACGAG
2311	TGAAGGCATCAACCCAGAGGATT	AAATCCTCTGGGTTGATGCCCTCA
2312	ACAGCTCGAAGGCAGCCACATTGG	CCAATGTGGCTGCCTTCGAGCTGT
2313	ACAACGAGTACCGCGACAGAAGGG	CCCTTCTGTCGCGGTACTCGTTGT
2314	ATAACCGAAAAACCAGCCTGCGAT	ATCGCAGGCTGGTTTCGGTTAT
2315	ACAACTCAGCACCTTCGACGTCCA	TGGACGTCGAAAGTGTGAGTTGT
2316	CGGGTTACTGGGTATACCAATGC	GCATTGGTATACCCAGTAACCCG
2317	CATCGGTTATCGCTGCACGCGCGT	ACCGCGTGCAGCGATAACCGATG
2318	GAAGGAATCCCGGATAGTCCGTGG	CCACGGACTATCCGGGATTCCCTTC
2319	GCATGGTCTCAGCAAAGAACCTG	CAGGTTCTTGGCTGAGACCATGC
2320	AGCCTGCGACGTTCCCGACAGAC	GTCTGCGGAAACGTCGCAGGCT
2321	AAGAAAGGCGCACGGGATCGATAT	ATATCGATCCCCTGCCTTCTT
2322	TGTCGCGAAGCAAATTCAAGTAA	TTACTGAAAGTTGGCTCGCGACA
2323	GCGGCATGCAAGGTAGGTCTGGAT	ATCCAGACCTACCTTGATGCCGC
2324	GGTGGCCATCTCCTCGAATTGCAT	ATGCAATTGAGGAGATGGCCACC
2325	GCGTGCATAAGTTGCACATTGTC	GCACAATGTGCAACTATGCACGC
2326	TTGAGGTAGCGTTTCGCGCATAT	ATATGCGCAAACGCTACCTCAA
2327	ATCCCACTTGTGAGAGGGCGCATT	AATGCGCCCTCTCACAAAGTGGGAT
2328	CGGTCAAGCGAGCAGACATCAACCT	AGGTTGATGTCGCTCGCTGACCG
2329	GCGTATCTCGGGTCGAACACTTG	CAAGTGTTCGACCCGAAGATACGC
2330	ATGCCATTGAACTCGCACTTGC	CGCAAAGTGCAGTTCAATGGCAT
2331	CGATTCCCATCATAATGTGGTCC	GGACCCACATTATGATGGGAATCG
2332	CAATTGGATAATCCAGCCACGCC	GGCGTGGCTGGATTATCCAAATTG
2333	CGGCTTACCCATGATTCCGTGCA	TGCACGGAATCATAGGGTAAGCCG

	2334	GGTGGACCATGCGCTGTGGTATGA	TCA TACCA CAGCGCATGGTCCACC
5	2335	TATTGTGCGAAGATCGCAAGCGCC	GGCGCTTGCATCTGACAAATA
	2336	GTCAGTGGGTTTGAGAGCCCCGA	TGC GGGCTCTCAAAACCCACTGAC
	2337	AGGGGGTCGGGAAATCTGACAAAA	TTTGTCA GATTTCCGACCCCT
	2338	TGCTTGCTATCCGAAAAAGCAGG	CCTGCTTTTCGGATAGCAAGCA
	2339	TTATCGGATCAAATTGGCTTCGG	CCGAAGCGAATTGATCCGATAA
10	2340	TGCAGCAACGAGTTACCGGACTT	AAGTCCGGTA ACTCGTTGCTGCA
	2341	TATACATGTCCGGAGGGGCACCA	TGGGTGCCCTCCGGACATGTATA
	2342	TGCAAAACCGGAGGATGAACCTT	AAGGGTCA TCCCTCCGGTTTGCA
	2343	TCGGTCTAATGTCCACGCAGACAC	GTGTCTCGTGGACATTAGACCGA
	2344	ATGTGTTGCCACCGCGCTCTATT	AATAGGAGCGCGTGGCAAACACAT
15	2345	TGGCGAGGCACGGCTTAATTGG	CCGAATTAGAGCGTGCCCTGCCA
	2346	GCGACGACCCGAGCGACTTTACA	TGTAAAAGTCGCTCGGTCGTCGC
	2347	CTCAGAGAGTCTATCCGGGCCCT	AGGGCGCCGGATAGACTCTTGAG
	2348	GGAACATCTCGTGGGCCCTCAGA	TCTGAGGGACCCAGGAGATGTTCC
	2349	GCAACGCAGGGAAAGTACTTAGCGA	TCGCTAAGTACTCCCTCGTTGC
20	2350	TGACTTGGCGGGACAAAGAACGC	GCGTTCTTGTCCGCCAAGTCA
	2351	AGATCATCGGGACGCTCATGCTA	TAGCATGAAGCGTCCCAGTGTCT
	2352	CCCTTCTGACCGCTAAGGCCATAA	TTATGGCCTAGCGGTAGAAGGG
	2353	CGTGAGCCGTGGGTGTCTGT	TACAGAGACACCCCACGGCTCACG
	2354	TACCTTGGTCGTCTCGCTTTGT	ACAAAAGCGGAGACGACCAAGGTA
25	2355	TCGCCGCAAAATGCTACGTAAAA	TTTCACGTAGCATTTGCGGCGA
	2356	GAGTGACCTAATGGCTGCCGACT	AGTCGGGCAGCCATTAGGTCACTC
	2357	AAAGGAACTTGGCCAACCCATGG	CCATAGGGTTGCCAAGTTCTTT
	2358	TGTTTCGCACTCCACCTAATCGC	GCGATTAGGTGGAGTGCAGAACACA
	2359	CAATGGGTTTCATAAGGGCAGGCA	TGCCTGCCCTATGAAACCCATTG
30	2360	GCCTAACACACAAGGGCCCTCTG	CAGAGGGACCCCTGTGTGTAGGC
	2361	CGTCATGCGGTCCGAGGATCGATC	GATCGATCCCTGGACCGCATGACG
	2362	CCACACGGGCACGGAGTAATATCT	AGATATTACTCCGTGCCGTGTGG
	2363	CATCAGACATAGGTGCGTGCAGA	TCGGCACCGCAGCTATGTCTGATG
	2364	AGATGAAACCAAGGGAGGACGCG	CTGCGTCCTCCCTGGTTCATCT
35	2365	GGCTACCCATAGGCTCAGCAGCAC	GTGCTGCTGAGCCTATGGGTAGCC
	2366	GGCTTGTGAGGGTGTGTTCTCGAC	GTCGAGAACACACCCCTACAAGCC
	2367	TGTGTTACGGCGAATGCAACAGTC	GAATGTTGCATTGCCGTAAACACA
	2368	CGATAACAGGTGCGGCCGTACTA	TAGTAACGGCGCGACCTGTTATCG
	2369	TGATAAAAGTGAGGCTCCAGCGCA	TCGCGCTGGAGCCTCACTTATCA
40	2370	AATTGTGACGGATCTGCACGGCG	CGCCGTGCAGATCCGTGCACAATT
	2371	GCAATGTACTGTCACCAGTGGCGA	TCGCCACTGGTGACAGTACATTGC
	2372	GGCATATCGGTAAACACTGGTCGG	CCGACCAAGTGTACCGATATGCC
	2373	GGGTCTAAACCAGCGTGGCCGCT	AGCGGCCACGCTGGTTGAGACCC
	2374	GTCTCCGGGACCATTGAGCTGGAG	CTCCAGCTCAATGGTCCCGGAGAC

	2375	GGCCTTCGGCATTCAAGACGGGTTG	CAACCCGCTCTGAATGCCGAAGGCC
	2376	CGTGATAGGCCACAGCGCTCAATT	AATTGAGCGCTGTGGCCTATCACG
	2377	GGCAGGCCCGCGAGGATGATTAAC	GTTAATCATCCTCGCGGGCTGCC
5	2378	CGGGTATGGTTGATAAACAGCGTGG	CCACGCTGTTATCAACCATAACCG
	2379	ACGACGTCTTGGGACCGTATTGT	ACAATACGGTCCCAGGACGTCGT
	2380	CTGATATCGAGCCTGAGCCTTCG	CGAAAGGCTCAGGCTCGATATCAG
	2381	TCCCATGGCCTGTATGCTGGCCT	AGGCCAGCATAAGGCCAATGGGA
	2382	GTGTCGTGATTGTTATCGACG	CGTCGATGAAACAATCGACGACAC
	2383	CGAAAGCCAGTAGCCGATTGCGTG	CACGCAATCGGCTACTGGCTTCG
10	2384	GGTCGGCTTATTCCACTGCGACA	TGTCGAGTGGAAATAAGCCGAACC
	2385	AGCGAGGGCTAACTTTAACGCG	CGCGTTAAAAAGTTAGCCCTCGCT
	2386	CGGCGCTGATGACGGGACTCGATT	AATCGAGTCCCCTCATCAGGCCG
	2387	TCACAGTGCCTGGCGTAAGGACTA	TAGTCCTTACGCCGAGCACTGTGA
	2388	CCCATTACGAGCACACACCATGGC	GCCATGGTGTGTGCTCGTAATGGG
15	2389	GGCCGCTAATCTTACGCATCACG	CGTGATGCGTAAAGATTAGCGGCC
	2390	ACGGCTTCCCTAGTGTCCAGCCCTT	AAGGGCTGGACACTAGGAAGCCGT
	2391	CTGTCAGGTCCCTACCCATGGCTC	GAGCCATTGGTAGGACCTGACAG
	2392	CACAGCCCATCCCACGACTGCT	AGCAGTTCACTGGGATGGCTGTG
	2393	ACAAACGATACCGAACGCTGTG	CACAGCGTTGCGTGTATCGTTGT
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	2395	ATCTCGAAACGATGCGTGCCTAAA	TTTAGGCACGCATCGTTCGAGAT
	2396	ATCTCGAGAACAGCGTGCCTCGG	CCGCACGCACGCTGTTCTCGAGAT
	2397	GAAGAAAATCCGCCGACATCTACGG	CCGTAGATGTCGGCGGATTCTTC
	2398	GCGGAGCAACCTTGGCTTTCTA	TAGAAACAGCCAAGGTTGCTCCGC
25	2399	CGCGTTCCGAAGACTTGTGTTTG	CAAACAACAAGTCTCGGAACCGCG
	2400	TGACCTGAAGCCCATTCCATAAGCA	TGCTTATGGATGGGCTTCAGGTCA
	2401	TGGTATTCTTCGGATAAGCGGG	CCCGCTTATCCGGAATGAATACCA
	2402	GCGTTGCAGGGTCTTGTGAAAC	GTTTGCATCAATGACCCGCAACGC
	2403	ACCGCTTCTGTGAGAGCCCTGA	TCAGGGCTCTACACAGAAAGCGGT
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	2405	TGTCCTGACAAATCAAGGTGCAGG	CCTGCACCTTGTATTGTCAGGACA
	2406	AAATTGCACTCGCGGAGATTCTCT	AGGAAATCTCCGCGAGTGCAATT
	2407	TGACGCCATTCTATATGGTGCA	TGCACCATATAGAAATGGCGTCA
	2408	TGTTCCGACAGGGACTGCTAGAC	GTCTAGCAGTGCCTGTCGGAACA
35	2409	TCGCTGGCTTGGGAAGGCCCTCGT	ACGAAGGCCCTCCCAAGCCAGCGA
	2410	GTGCACCTCCGTTGGCTAGAATG	CATTCTACGCCAACGGAGGTGCAC
	2411	CTCATTGGGACCGATGGGTTGC	GCAACCCGATCGGTCCCAAATGAG
	2412	GCCAGTGTCTGTCAATGGATGGGA	TCCCCATCCATTGACAGACACTGGC
	2413	TTGCCCGGCAGGTTCTGTGTAATG	CATTACACAGAACCTGCCGGCAA
40	2414	ACCCGCGAACCGAGACGCACTTCT	AGAAGTGCCTCTCGGTTCGCGGGT
	2415	TCCGTGCGATTGGTCAAGGTTGAT	ATCAACCTTGACCAATCGCACCGA

	2416	AGGGCGTCTCGGTTAACCTCGGT	ACCGAGGTTCAACCGAGACGCCCT
	2417	TGACCGTTCAAAGAGCAAGCCAAC	GTTGGCTTGCTCTTGAACGGTCA
	2418	ACACTCACCTGCTGCCCTGCTGA	TCAGCAGGGACAGCAGGTGAGTGT
5	2419	GCGTTAACCTCTGGGTGGTGGT	ACCACCAACCAAGGAGTTAACGC
	2420	CGCCTGCGCAGGTAACCTCCGCA	TGCGGAGAGTTACCTGCGCAGGCG
	2421	AATCGAATTCCCAGCGGCTGTTT	AAACAGCCGCTGGAAATTCGATT
	2422	AAGCAGGTGGGATCCTGGGATCA	TGATCCCCAGGATCCCACCTGCTT
	2423	AATCCCAGACTCGCTTCTCGTGT	AGCACGAAGAGCGAGTCTGGGATT
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	2425	TACGAGAGCGGGCTTAGACGTCGC	GCGACGTCTAAGCCCGCTCGTA
	2426	GCGATTTGACCCACGGTTATCGA	TCGATAACCGTGGGTCAAAATCGC
	2427	AGCTGTATAATTGGATGGCGCGA	TCGCGCCATCCAAATTATACAGCT
	2428	TCCGCGAGTCTTAGCCGATTGAAC	GTTCAATCGGCTAAGACTCGCGGA
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	2431	GCGAGCCTTTGCTGGGAAGAG	CTCTTCCCAAGCAAAAGGCTCGC
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	2433	CGGGTCGACCCCTGAAGCATAACC	GGTTATGCTCAAGGGTCGACCCG
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	2435	GCAGTCCTATCCGGAGCCTGACAA	TTGTCAGGCTCCGGATAGGACTGC
	2436	AAGGTGCGCTATTGTTGTCGGTC	GACCGACAACAAATAGCGCACCTT
	2437	AGTGAATCCATGCCGACACCTGA	TCAGGTGTCGGCATGGATTCCACT
	2438	TACAGGCGTAATTCTGCGAGGGG	TCCCTCGCAGGAATTACGCTGTA
25	2439	CCGAAGTGCAGAGAACGACGTT	AACAACTGCTTCTGCACTTCGG
	2440	AAGGACTGGTATGGCCGGAGCTT	AAAGCTCCGCCATACAGTCCTT
	2441	GGACACCGCCAACCTCATAGTTC	GCAACTATGAGGTTGGCGGTGTCC
	2442	AATGGTGTTCGCCTGGACTACCAC	GTGGTAGTCCAGGCCAACACCATT
	2443	TAGGAAAGCGTACACGGGAATCCG	CGGATTCCCGTGTACGCTTCCTA
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	2445	CGTGTCCGTGTGACACTGTCCATG	CATGGACAGTGTACACGGACACG
	2446	TCCAGGCTTGCAGTACGGTAG	CTACCGTATCCGCAACAGCCTGGA
	2447	GTAGGCCAAATGGTCGCGATCAAT	ATTGATCGCGACCATTTCGCTAC
	2448	ATCTCCGTGGACCCGATTGTGACA	TGTCACAATCGGGTCCACGGAGAT
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	2450	TTCCGGAAAGCGTTGGTAACCTTG	CAAAGTTACCAAACGCTTCCGGAA
	2451	TTCGATAGGAATACCAAGGGCTGG	CCAGGCCCTGGTATTCTATCGAA
	2452	GGCCATTGAGGAGGATTATGCAA	TTGCATAATCCTCCTCAAATGGCC
	2453	ACCTTCTGACCTGGACTTTGGCG	CGCCAAAAGTCCAGGTAGAAGGT
40	2454	GACCAATCCGCAAGTTGAGCAACAG	CTGTTGCTCAACTGCGGATTGGTC
	2455	TCGGCCACTCACCAGTGTAGG	CCTACACTCATGGTGAGTGGCCGA
	2456	AGCGCTCACATGTTGAAAACGGG	CCCGTTTCGAACATGTGAGCGCT

	2457	TAACGCAAAGGCAGCGATCCCGCT	AGCGAGGATCGCGCCTTGCCTTA
	2458	TGGGTGGGCCAAATATTACTGCAA	TTGCAGTAATATTGGCCCACCCA
5	2459	GTCCTCGAAAGGGGCATCCAAACA	TGTTGGATGCCCTTCGAGGAC
	2460	CCCATCTGGTGGGAGGCCTATCA	TGATAACGCCCTCCACCAGATGGG
	2461	GTGCGCGGTCTGCAAACCTGCCAT	ATGGCGAGTTTGCAAGACCGCGCAC
	2462	TGTGTTGCCAACCCTAGGTATCA	TGATGACCTAGGGTTGGCAACACA
	2463	CTGATGCTGTTCTCGTCGGTTGAC	GTCAACCGACGAGAACAGCATCAG
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	2465	TCTGACGCCGTGCTGGGAGTCTAT	ATAGACTCCAAGCACCGTCAGA
	2466	GAATTACTGGAGGCAGCGCTGCAA	TTGCACGGCGCCTCCAAGTAATT
	2467	GATTCTTCCCAGCCTAGGTTGGCC	GGCCAACCTAGGTGGGAAGAACAT
	2468	CGCAGCGTATCCCAGTGTGCTTGA	TCAAGCAACATGGGATACGCTGCG
	2469	GAGATGGAATTGTTGCCCAAAGA	TCTTTGGCGAACAAATTCCATCTC
15	2470	GATGCCCTGGATCGGTCTAGCGTCA	TGACGCTAGACCGATCCAGGCATC
	2471	GCAGCGACTGCTAACGCTATCTCGG	CCGAGATAGCTTAGCAGTCGCTGC
	2472	AGGGCTAATTACATGCCCTGCC	GGCAAGGGATGAAATTAGCCCT
	2473	AAGTGCACATCCTCACGAAGCGAT	ATCGCTTCGTGAGGATGTGCACTT
	2474	TCAGGCAGCCGTAAATTAAATGCGC	GCGCATTTAATTACGGCTGCCCTGA
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	2476	TTGTCCAAAGCCACCTACGACAGA	TCTGTCGTAGGTGGCTTGGACAA
	2477	TGGGCGGAATAGATTGGGTGCTT	AAGACACCCAATCTATTCCGCCA
	2478	TAGAATTGCCCTTCTAGCCGCC	GGCGGCTAGAAGAGGCGAACATTCTA
	2479	CATTACTCCTGCAGATGCGATGC	GCATCGCATCTGCAGGAAGTAATG
25	2480	GGAAATGCTAGCTGGGTAATCGC	GCGATTACCCAGCTAGCATTCC
	2481	GCCGCCACTGCGAATCTACATCT	AGATGTAGATTGCAAGTGGCGGC
	2482	ACAATAGCGGACAGCTGCCAGAT	ATCTGGCGAGCTGTCGCTATTGT
	2483	AGTTAGGCTCTCGGTGCGGTCCAT	ATGGACCGCACCGAGAGCCTAACT
	2484	TGGGCCTGAGAAGCGGTTAATAGG	CCTATTAAACCGCTTCTCAGGCCA
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	2486	CCTGGTGATCGTGTCCCAGACTCA	TGAGTCTGGGACACGATCACCAGG
	2487	GCGTGTCCATTGCTTGAGGTTTC	GAAACCTCAAGCGAACGGACACGC
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	2489	TTACGTTCTCACCGATCAACGCC	GGCGTTGATCGGTGAGAAACGTAA
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	2491	ATCTACGATGCGGCTCGAACGT	AAACACTTCAAGCCGATCGTAGAT
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	2493	AACTGCGGTGGTGGAGGCAGGTGC	GCACCTGCCTCCACCACCGCAGTT
	2494	TGCGATCTCTCCACCTACAGCGC	GCGCTGTAGGTGGAGAACATCGCA
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	2496	TGGAAAATTGGGAAACGCTGGA	TCCAGCGTTCCAAAATTTC
	2497	CCAGCGCCGCACCTCTCCAATAG	CTATTGGAGAACGGTGCAGCGCTGG

2498	TAGACGGCTGGCGAATCTTACGGT	ACCGTAAGATTGCCAGCCGTCTA
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2500	G TAGCCGAGAGCAATTTCACCGC	GCGGTGAAAATTGCTCTCGGCTAC
2501	GCAA ACTCCCCTGCCCTTAGCCT	AGGCTAAAGGGCAGGGAGTTGC
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2508	GATT TATTGGCGCGGTAACGACCT	AGGTCGTTACCGCGCCAATAAAC
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2520	ATTCAGACCTCGGGACAACCTGG	CCAGGTTGCCCCGAGGTCTGAAAT
2521	GAAGTGC CGTAACTTAGGGAGCC	GGCTCCCTAAGTTACGCGCACTTC
2522	TTGGCCAGGT CATCACTCTGCCAT	ATGGCAGAGTGTGACCTGGCAA
2523	ATCGGCCGGTATTAGCTGCCCTCC	GGAGGGCAGCTAATACCGCCGAT
2524	CGCAGGTAAAGCCGAGCAATGTT	AAACATTGCTGGCCTTACCTGCG
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2532	ATTGCCGCGTCTCGTATCAAAGA	TCTTTGATACGAGACGCGGCAAT
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2536	TCGCATACTCGTCGGCGAGTATT	AATACTCGCCGACGAAGTATGCGA
2537	CGTGAGCCGTTCTCATCCAAGCGG	CCGCTGGATGAGAACGGCTACG
2538	GCAGAATCGAATTGGGTGGTTT	AAACCCACCCAAATTGATTCTGC

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	2540	GACCAGTTAGTGCAATGGTGGCG	CGCCAACCATTGCACTAAGTGGTC
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	2547	TGCACCTGTCTGTAGATTGGGT	ACCGCAAATCTACAGACAGGTGCA
	2548	CATAAAGCACGGACGCGACTTGAT	ATCAAGTCGCGTCCGTGCTTATG
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	2553	CCTGCTGGTTCGGTCGTAAGCGAA	TTCGCTTACGACCGAACCGAGCAGG
	2554	GAGGCACCAATCGGTCTGAAAATG	CATTTTCAGACCGATTGGTGCCTC
	2555	TACGAAAATGGTTCGGCCGGTCT	AGACCCGGCGAACCATTTCGTA
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	2562	GCCACATTCTGCTACCTCCGTGTT	AAACACGGAGGTAGCAGAACATGGC
	2563	TCCTGTGCTTGTGACGTGCTAGG	CCTAGCACGTACAAAGCACAGGA
	2564	GACCGCATATACACCTGATGGCC	GGCCCACATCAGGTGTATATGCGGTC
	2565	GTAGGCCCGTCGTTAACCATCTCA	TGAGATGGTTAACGACGGGCCTAC
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	2567	GCTGATCGGCTTTCACCGCTATA	TATAGCGGTGAAAAGCCGATCAGC
	2568	TATCAAATCGTGGCACCGCACTA	TAGTCGCGTGCCAACGATTGATA
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	2574	CACTCCGTCTCGTCCATTAATGCG	CGCATTAAATGGACGAGACGGAGTG
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	2576	GAATCAATTTCAGGGACGGGAC	GTCCCGTCCCTGGAAAATTGATTC
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5	2582	CATCATCCACACAGGCAGGTGTGT	ACACACCTGCCTGTGGATGATG
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	2600	CGAATTGATAGCGTTACGGGCAA	TCGCCCCGTAACGCTATCAATTG
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	2604	TCGGTGATTGTAATTGGATCCG	CGGATCCAAATTACCAATCACCGA
	2605	GCGGGCAGGTAGTTGACTGGATG	CATCCAGTCAAACTACCTGCCCGC
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	2609	CGCGGCAAAGATTAATTCCGGCG	CGCCGGGAATTAAATCTTGCAGCG
	2610	GAAGACCCGTCCGGTTCCATAC	GTATGGAAACCCGGACGGGTCTC
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	2612	CTGTGCAGGGGGTGGCTCTGTTGA	TCAACAGAGCCACCCCTGCACAG
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	2615	CTGCCACCATCTACGGCGAGTCT	AGACTGCCGTAGATGGTGGCAG
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	2617	AATTCAAGACGCCACATCGACGGTC	GACCGTCGATGTGGCGTCTGAATT
	2618	CCGTGGTCTGCCCTCGATTACCTAC	GTAGGTAATCGAGGCAGACCACGG
	2619	GGCGAGGAATTGGAACCTTATG	CATAAGGTTCCGAAATTCTCGCC
	2620	ATCCGATGATCAGATACCGGCTGG	CCAGCCGGTATCTGATCATCGGAT

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2624	GGGATTGGCTTGGTGGAAAGAA	TTCTCCAACCAAGAGCCAATCCC
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2637	CCGTTAGTGGTCGACAGTCGGTT	AACCGAACTGTCGACCAACTACGG
2638	TCAGGCTACGCCCTCAGCACTACA	TGTAGTGCTGAGGGCGTAGCCTGA
2639	TATACGGGCCGAGGTCCGTATTCG	CGAATACGGACCTCGGCCCCTATA
2640	CCAACGTGTGACGAAGGGCCATTG	CAATGGCCCTTGTACACGTTGG
2641	CTGCTCAGCGGTGCTTAAAGACA	TGTCTTCAAGCACCGCTGAGCAG
2642	GGAGATTGACTTCGCGTTACCA	TGGTGAAACCGGAAGTCAATCTCC
2643	ATGGTTCAAGGTTCTCGTGGGTT	AACCCGACGAACCTCTGAACCAT
2644	GAGTGGAGCATTCTCGGCCCTCAA	TTGAGGGCCGAGAATGCTCCACTC
2645	TGGATTGGAACCAATCCCGACAA	TTGTGCGGATTGGTCCAATCCA
2646	TGCTCTTGTGGTCACTCGAGAGGA	TCCTCTCGAGTGACCAAGAGCA
2647	TTGGGAGCACGGTTACCGCCTGTG	CACAGGCAGTAACCGTGCTCCCAA
2648	CAACCGCAGCTAACGGTAGTTCG	CGAAACTACCGTTAGCTCGCGTTG
2649	AACGCTGAGCGCTCACCTCACCT	AGGTGAAGGTGAGCGCTCAGCGTT
2650	CCGTCGTAGATCTGGAGGCTCAA	TTGAAGCCTCCAGATCTACGACGG
2651	GGATGGCATGGGCACACTGTAACC	GGTTACAGTGTGCCCATGCCATCC
2652	TCGTCGTAGATATCCTCACGCC	GGCGTGAAGGATATCTACGAGCGA
2653	GGAGCAATACCGCGTCCAAAACAC	GTGTTTGAGCGCGGTATTGCTCC
2654	TTGTTCAAGACTAGGCCTGCCCA	TGGGCAGCGCTAACGTTGAACAA
2655	CGGCGGTACTCTTCCACTGTCTT	AGGACAGTGGAAAGAGTACCGCCG
2656	AAGACGATTGCCACGTGCCAGAG	CTCTGGCACGTGGCAATCGTCTT
2657	AGGTGAGCGCAGGCATATTGCACT	ACTGCAATATGCCTCGCGCTCACCT
2658	CTCGGGCCTGTACAGCAAAGCCGT	ACGGCTTGCTGTACAGGCCGAG
2659	TGCGCGCTAGTGCTGCCTATGATC	GATCATAGGCAGCACTAGCGCGCA
2660	CCATCCTTGCCTTGAGGTAAGG	CCTTACCCCTCAAGGCAAAGGATGG
2661	AACAAACAGCGTAAGACGGACAGGG	CCCTGTCCGTCTACGCTGTTGTT

	2662	GAGGCGGTGAGGGCTACAATATT	AATATTGTGAGCCTCGACCGCCCT
	2663	CGAGGTTAGACGCCATGACCCAC	GTGGGTCAAGGCCTAACCTCG
5	2664	AACTTGCTATACCGGCGCAGCAA	TTGCTGCCCGGTATAGCAAGTT
	2665	CGCGGTGAATCGCATACACAGCGC	GCGCTGTATGCATTACCGCG
	2666	CACCGAATCAAGCCATATGGCTCT	AGAGCCATATGGCTTGAATCGGTG
	2667	TTCACAGCTATCCTAGGCGCTGCC	GGCAGCGCCTAGGATAGCTGTGAA
	2668	AGAACGCGAAGTGTACCCCGCAT	ATGCGGGGTACACTCGCGCTTCT
10	2669	TGCATGGTATTGCGTGCGATAGG	CCTATCGCACGCAAATACCATGCA
	2670	GGCCGGACCTATGTGAGATGGAAA	TTTCCATCTCACATAGGTCCGGCC
	2671	TCAACCTGAGCCTGATCCCAAGC	GCTTGGGATCAGGACTCAGGTTGA
	2672	TGCTTACCGTTCAAGGGAGGCGTGT	ACACGCCTCCCTGAACGGTAAGCA
	2673	GGAGAGTTACCGATGAGCCACCT	AGGTGGCTCATCGCGTAACTCTCC
	2674	CGGTATCGGGTGTACAGCTTCGT	ACGAAAGCTGTACACCGCATAACCG
15	2675	GTAAGCCGGGTCCTCGTGTGCCGT	ACGGCGACACGAGACCCGGCTTAC
	2676	GCGTAGTGCACGCCCGACCTA	TAGGTCGGGCGTTCGCACTACGC
	2677	TCCTCGCGCTTACGTCAAATTG	CGAATTGACGTAAGCCGCGAGGA
	2678	CGACGTTCAAAGCGGGAGAGGAGG	CCTCTCTCCGCTTGAACGTCG
	2679	CGAGGCACCCCGACATGTTGAGAT	ATCTCAACATGTCGGGTCGCTCG
20	2680	CTATTCGTGCCCGTCGGACAAG	CTTGTCCACGCGGGCACGAAATAG
	2681	GGCTGCTCAGTGACGGTGTCAACTG	CAGTTGACACGTCACTGAGCAGCC
	2682	ATCACTCGTGCCTACCGACCGTC	GACGGTCGGGTACGCACGAGTGAT
	2683	CGAGATGTCCTATACCGTGGCGAA	TTCGCCACGGTATAGGACATCTCG
	2684	TCACACCGAGCCCCATAATGAAA	TTTCATTTATGGGGCTCGGTGTGA
25	2685	AGCTACGTGTCAGCAGAAAGCG	CGCTTTGCTCGAGACACGTAGCT
	2686	TCAGGGCGAGTTTTTCAGCGCG	CGCCGCTGAAAAAAACTCGCCCTGA
	2687	TTCGTTCTGTCTATTTGCCCG	GGGGGCAAAATAGACAGAACGAA
	2688	TGGTATGCCCAAGGATCCAGCCTAC	GTAGGCTGGATCCTGGGCATACCA
	2689	TCTCAGTCGTTAGGCCATGGCGG	CCGCCATTGGCTAACGACTGAGA
	2690	AAAGATCACCCTGGAGCGATCGGC	GGCGATCGCTCCACGGTGATCTT
30	2691	TAGCAGGACTTGCACTCGTATGC	GCATCACGAGTGCAAGTCCTGCTA
	2692	TGCCCACGGTACCGTTCAAGGCTG	CAGCCTTGAACGGTACCGTGGGCA
	2693	TGAGGTGCGTCGCCCTAACGATG	CATTACTTAGGGCAGCGACCTCA
	2694	AGCAAGGGTTACAACCCGCAACCC	GGGTTGCGGGTTGTAACCCCTGCT
	2695	CACAACAGCCAGTATTGCCACAA	TTGTGGCGAATACTGGCTTGTG
35	2696	GGCAACACCACTCGACGAGCTC	GAGCTCGTCGAGTATGGTGTGCC
	2697	GGCTGGATTGACAATTAGCCCCT	AGGGGCTAAATTGTCATCCAGCC
	2698	CGTGAGAAATGCTACACCGCTAG	CTGACCGCTGTAGCATTCTCACG
	2699	CGCATCTGCCCTAACGGTCTT	AAGGAACAAAATGGGGCAGATGCG
40	2700	GTCGGCCTAGTCGGCAGAACGGTG	CACCGTTCTGCCGACTAGGCCGAC
	2701	TCCCTCACCTCCAAAAATGTGCT	AGCACATTGGAAAGGTGAGGGAA
	2702	GGGCAAGAACATGAGAACAGACCG	CGGTCTGTTCTCATGTTCTGCC

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2703	TCGTCCCTGGTACGACTTGCCTAGA	TCTACGCAAGTCGTACCAGGACGA
2704	TGGCGGTTGCATGTGATGATCAAG	CTTGATCATCACATGCAACCGCCA
2705	CCTCGCGTGGAGTAAAAACCGTCCG	CGGACGGTTTTACTCACCGGAGG
2706	ACTTCCGCCAACAGAACAGGGCCAG	CTGGCCGCATTCTGGCGGAAGT
2707	GTGTAGAGCTGGTAGCCCCGTT	AACGGGGCTACCCAAAGCTACAC
2708	CGCAGCATCCGAGTTAACACACAT	ATGTGTGTTAACTCGGATGCTGCG
2709	ATGAGCCTGGATGATCCGCTGGT	ACCAGCGGATCATCCAGGCTCAT
2710	CCTGGCATAAGTGCCGACATGCTT	AAGCATGTCGGCACTTATGCCAGG
2711	GCGCATGAAAAACTACGACGGACG	CGTCCGTCGTAGTTTATGCCGC
2712	AAAGATGGTCGATGGGAGCGTCT	AGACGCTCCCCTGACCCATCTT
2713	ATCCTGGGACGAGCGGATTATC	GATAAAATCCGCTCGTGCAGGAT
2714	TCACCGCATTGATAGTTACGCGA	TCGCGTAACTATCAAATGCGGTGA
2715	TGGTGGAGCGGACTCTGGTGTAT	ATAACACCAGAGTCCGCTCCACCA
2716	CACAATGAAAAAACAAATGGCCCCA	TGGGGCCATTGTTTTTATTGTG
2717	CCTTGCCGCGCTTGTGGTACCAAC	GTTGGTACCCACAAGCGCGGAAAGG
2718	CCGAGACCTTGCCACACGAAAGA	TCTTCGTGTGGCAAAGGTCTCGG
2719	ACCGCGGTGTACACCTGAGCAGGC	GCCTGCTCAGGTGTACACCGCGGT
2720	GTCGTACGCTTACCGCAGCGGAGA	TCTCCGCTCGGTAAGCGTACGAC
2721	TCGTAATTGACCGACACACGCAG	CTGCGTGTGTCGGTCAAATTACGA
2722	CCTAGACGGATAACCTGAGCGGAA	TTCCGCTCAGGTATCCGTCTAGG
2723	AAGCGACAGCAGAGGTTAGTCGC	GCGACTGAACCTCTGCTGTCGCTT
2724	GCGTGGACGATATCACCTGGCGT	ACGCCCAGGTGATATCGTCCACGC
2725	GTCGGAGAGCCAGTGGTACGGCTT	AAGCCGTACCAACTGGCTCTCCGAC
2726	TATCCGCACGGTATAGCAGTTGCA	TGCAACTGCTATACCGTGCAGATA
2727	CATCAGTCGGCTACCTCAGCCT	AGGCTGAAGGTAGCCCAGTGTG
2728	CGGATTAATGCCCTTCCTCGGAAT	ATTCCGAGGAAAGGCATTACCG
2729	TTCGTCGTGCCAAGCTAATGCAAG	CTTGCATTAGCTGGCACGACGAA
2730	GGCCGAGACCACCAAGAACAGGTT	AACCTGTTACTGGTGGTCTCGGCC
2731	CGCGCGGAAGCATTGAAGTTACTA	TAGTAACCTCAATGCTCCGCGCG
2732	TCGGCTTACCGCTTCTGACTT	AAGTCAGACGAAGCGGTAGCCGA
2733	GACTGACGTCAAGGCAAGAACAC	GTGTTGCTGCCTGACGTAGTC
2734	AGAGGAAGGAGGGCTGTGACAGA	TCTGTCACAGCCCCTCTTCTCT
2735	TTCCAATGCGAGAGATGGCAGGCT	AGCCTGCCATCTCGCATTGGAA
2736	AAATGGGTGCTCGAATATGTCG	CGACATATTGAAGCACCCATT
2737	GCTGTCGGATTATTGCACGCCGT	ACAGGGCGTGAATAATCCGACAGC
2738	CCGACTTTGTTATGTTGCTGGCG	CGCCAGCAACATAAACAAAGTCGG
2739	GCTGCGATATAACCGTCCCAGAA	TTCTGGGACGGGTTATATCGCAGC
2740	TGAGCTGGCGTCAACTCCGAAGA	TCTTCGGAGTTGACGCCAGCTCA
2741	CCCAAGCATCCTAAATCTCCCTCG	CGAGGGAGATTAGGATGCTGGG
2742	CGACAGCAATCCACATGCATTCTT	AAGAATGCATGTCGGATTGCTGTCG
2743	TGAATGGTCGGAAACCAATGCAT	ATGCATTGGTTCCGACCATTCA

	2744	CTTTCATCGAGATGCGGGGTAGC	GCTACCCCCCATCTCGATGCAAAG
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	2746	CCACTACGCCATCCTGACAACGAG	CTCGTTGTCAGGATGGCGTAGTGG
	2747	TAGTAAGGCCAATGTACGCCGTCC	GGACGGCGTACATTGGCCTACTA
	2748	GTCATGCATATGGGCCCTGTTTC	GAAAACAGGCCCATATGCATGAC
	2749	ACCGGTAGACGTTAGCGGGTCAA	TTGAACCCGCTAACGTCTACCGGT
	2750	TTGGTCAAACGGCCACACGTCTC	GAGACGTGTGGCCGTTGAACCAA
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	2752	CTCGAGCGCTGTCAATATCGGC	GCCGATATGATGACAGCGCTCGAG
	2753	GCGGCTAAGGCACAAGTAGACGTG	CACGTCTACTTGTGCCCTAGCCGC
	2754	ACAGCCTAAATGGCGCAAGACCGA	TCGGTCTTGCGCCATTAGGCTGT
	2755	CCGATGATGTAAGCCGTCGGCCCT	AGGGCCGACGGCTTACATCATCGG
	2756	AGGAGCAAACAAACGCCAGTGACA	TGTCACTGGCGTTGTTGCTCCT
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	2758	CTGTTCCAGTTGGCAAGTGGGC	GCCGCACTTGCCTGAACGGAAACAG
	2759	AGACAAGTCAGGAACCGCGTTCCG	CGGAAACCGCTTCCCTGACTTGTCT
	2760	AGACGACGGCCAGATACTGCTGCCA	TGGCAGCGTATCTGCCGTGTCCT
	2761	AGGAAGCGCTTCTCCGGTTCTC	GAAGAACCGGAAGAACCGCTTCC
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	2763	CGCATAGCAGTCTCCGCATCTGG	CCAAGATGCGGAGACTGCTATGCG
	2764	TGGTTCCGGTGTGCAACAGATAAA	TTTATCTGTTGCACACCGGAACCA
	2765	CCGTATGCCACCTCCAGAACTCAA	TTGAGTTCTGGAGGTGGCATACGG
	2766	GTAAAGGAACCCCTCGGAATCCT	AGGATTCCGAGGGGTTCCCTTAC
25	2767	GCCTGATGCTGTTAAAATTGCGT	ACGCAATTAAACGAGCATCAGGC
	2768	TCGCACTTGGACCATGAGATCTGA	TCAGATCTCATGGTCCAAGTGCAG
	2769	TTCTCAGGCTGGGCAAGAGTCTGT	ACAGACTCTTGCCTGAGAA
	2770	CGGACCTGGGATGCTGGATTAC	GTAATCCCAGCATCCCCAGGTCCG
	2771	TCGAGCCGATAGGGTTGGCATTGC	GCAATGCCAACCCATCGGCTCGA
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	2773	TGTGAAATTGCGTTTCGCATCTT	AAGATGCGAAACGCGAATTTCACA
	2774	TTGCAATGCTCCAAAAAAACTGCC	GGCAGTTTTGGAGCATTGCAA
	2775	TCTCATCATGGCTGGCTTGAC	GTCAAAGCCACAGCCATGATGAGA
	2776	ATTACACCGCTTGGTTGGAGTGG	CCACTCCAAACCAAGCGGTGTAAT
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	2778	GAGATCAGACCGTGTGGATGCTG	CAGCATCCGACACGGTCTGATCTC
	2779	CCACCTATCTGATGCGACCTGGA	TCCAGGTGCGCATCAAGATAGGTGG
	2780	CCGATGCCGTTATGTCTACGGC	GGCGTAGACATAACGGCGATCGG
	2781	AAAAATCACGGTAAGGCACGTTCG	CGAACGTGCCCTACCGTGATTTC
40	2782	GATTCTCGCTCCCAACGAGCATA	TATGCTGTTGGGAAGCGAGAATC
	2783	TGTGAAATGTGGCAGTCTCAGGG	TCCCTGAGACTGCCACATTTCACA
	2784	CGATCCTGCGTGCCTCATCCAGGC	GCCTGGATGAGGCACGCAGGATCG

	2785	CCCTCAAGTGGCGAGGGTTCA	TGAAAACCTCGCCCACTTGAGGG
	2786	TCGCCTCCGCCCTCGTGTAGAAG	CTTCTACACACGAGGCGGAGGCAG
5	2787	TTCGCTTCAGCTCATTGAAACGA	TCGTTCCAATGAGCTGAAAGCGAA
	2788	TGTAATCTGAACAAGCGGACCCCT	AGGGGTCCGCTTGTTCAGATTACA
	2789	TGGAATCTTCTTGAGCGCCGTGA	TCACGGCGCTCAAGAAAGATTCCA
	2790	GGCTTCATCTTAACCGCTCGGT	ACCGAGCGGTTAAAGATGAAAGGCC
	2791	TGATCCGAGCCATTCTAATCACC	GGTGATTAGGAATGGCTCGGATCA
	2792	TGGTAGGCGTGATGTCCTACGCAA	TTGCGTAGGACATCACGCCATCCA
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	2795	ACATGGACGAAATTACGCCGTCA	TGACGGGCGTAATTCTGTCATGT
	2796	ACAGAAAGGTGGGAGCCTAGCGT	ACGCTAGGCTCCCCACCTTCTGT
	2797	AGGCTTGCACATGGTAGTGCAC	GTCACTACCCATGTCGCAAGCCT
15	2798	GCGTGGGCCTTGCTCTGTTAAC	GTTAACACAGGAGCAAGGCCACGC
	2799	GAATACAGAGCGTCCGATGTGCC	GGGCACATCGGACGCTCTGTATT
	2800	GCGACTCTGTAGGGAGCGCGATAT	ATATCGCGCTCCCTACAGAGTCGC
	2801	GGTGCACTCATATGCGTCGCATCG	CGATGCGACGCATATGAGTGCACC
	2802	CTGTCACGGGAAACCTTACTT	AAGTAAGGTTCCCCGTGGACAG
20	2803	TGGCTTACTGTCGCAATCTAGGCC	GGCCTAGATTGCGACAGTAAGCCA
	2804	GCACTCAGTTCCGGTATCCCATG	CATGGGATACCGGAAACTGAGTGC
	2805	GTGAGGTTACGTAAGGACAGCG	CGCTGTGCCCTACGTGAACCTCAC
	2806	GTAACGCCCTTGTCCCCAGCGTAT	ATACGCTGGGACAAAGGCATTAC
	2807	GCATTGATATGGTCGGTCTCGCCT	AGGCGAGACCGACCATAATCAATGC
25	2808	GTGGGTTAAAGTGACAACGGACGC	GCGTCCGTTGTCACTTAAACCCAC
	2809	CAAAACCTGCCGAAGATGTTGGT	ACCAACATCTCGGCAGGGTTTG
	2810	TCCGAGGAGACTGAACCTGCTACC	GGTAGCAGGTTACGTCCTCGGA
	2811	CGGGGAAGAACGGATTGCTAAAT	ATTTAGCGAATCGTTTCCCCG
	2812	TGGTTAGCTTATGTCGGAGCCACC	GGTGGCTCCGACATAAGCTAACCA
30	2813	ACCGCGTCGATGAACTAAGGCTCGC	GCGAGCCTTAGTTACGACCGGT
	2814	TTCTCCTGACGAGTACGCAGTGGG	CCCACTGCGTACTCGTCAGGAGAA
	2815	TCCGCGGTTGCCGGTTGTTAGGA	TCCTAACAAACCGGCAACCGCGGA
	2816	TGGCGCATCTTCAGGGGATGATG	CATCATCCCCGAAAGATGCCCA
	2817	TCTTGGTCCTGGTGTACGCG	CGCGTAAACACCAAGGACCAAGA
	2818	GAGAACTCCGCTACAAAGGAGCC	GGCTCCTTGTAGCGGGAGTCTC
35	2819	TTAACGTGGAACCGTTGGTGAAT	ATTCACCAACGGTCCCACGTTAA
	2820	GGGACACCATCCTGGGTTGTTA	TAACAAACCCAAGGATGGTGTCCC
	2821	CAACAAACCGCCTGGGAAGTGAC	GTCACCTCCAAGGCGGTTGTTG
	2822	TTGAAGGCCACCGATACTGATCGC	GCGATCAGTACGGTGGCCTCAA
	2823	TCGTAATAGAACTGCGCCAATGC	GCATTGGCGCAGTTCTATTACGA
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	2825	ACATAGCTGGCCGGACACCCACC	GGTGGGTGTCGGCCAAGCTATGT

	2826	CTTGGCCGCTTGCGAGTGGCTAAA	TTTAGCCACTCGCAAGGCAGGCAAG
	2827	AATGGCTGCCAGATACCGCAGCC	GGCTGCGGTATCTGGCGAGCCATT
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	2829	CGTCCACTTAGGTGGAGATACGCC	GGCGTATCTCCACCTAAGTGGACG
	2830	GAGCCTCTCGTCCTGAAGACCGA	TCGGTCTTCAGGACGAAGAGGCTC
	2831	AACATCAAGCGGCAATCTCCCTC	GAAGGGAGATTGCCGCTTGATGTT
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	2833	TGTGCAGACCCTAACGACCTACGG	CCGTAGGTCGTTAGGGTCTGCACA
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	2838	CAGTTTCATTGCAGCGAAAGCAA	TTGCTTCGCTGCAATGAAAATG
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	2840	CATCCGGCCTCAGTGATTCTTACC	GGTAAGAACACTGAGGCCGGATG
	2841	TGCTGGAAGCCACAAACGTTACGT	ACGTAACGTTGTGGCTTCCAGCA
	2842	GAACGGCCAGGGGACAACATCGT	ACGATAGTTGTCCTGGCGTTC
	2843	TCATCTAGGTCGAAGCGCAAGACA	TGTCTGCCCTCGACCTAGATGA
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	2846	GCCAACAGGAGATGCTGCACCAT	ATGGTGCAGCATCTCTGTTGGC
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	2848	GGTCGCGTAGT GAGTCAGAGGC GT	ACGCCTCTGACTCACTACGCGACC
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	2850	TATACAGCATCGTCGCCGGGCATA	TATGCCCGCGACGATGCTGTATA
	2851	GCTTAGTGGCGTCTCGTCGTAGG	CCTACGACGAAGACGCCACTAACG
	2852	TGCACTCCGCAACCTTGAAATC	GATTTACAAGGTTGGGAGTGCA
	2853	AACCCGTATGCCGACTCCATCTA	TAGATGGAGTCGGCATGACGGGTT
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	2857	TTCTGCTATGCCGTATGGGGGCCG	CGGGCCCCCATACGCATAGCAGAA
	2858	CGAACTACTGCGTCAGCCTCTCC	GGGAGAGGCTGACGCAGTAGTCG
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	2860	ATAAACAGTGGCAATGAGCGGAA	TTCCCGCTATTGCCACTGTTATT
	2861	ATATGTTGATTCCC GTGCTGCACA	TGTGCAGCACGGGAATCAACATAT
	2862	AGAGTGGGCACCACCAAGGCAGACA	TGTCTGCCCTGGTGGTGCCACTCT
	2863	AGGCCTGGGTTCTGCGTCTTAGT	ACTAAGACGCAGAAACCCAGGCCT
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	2867	CAGGACGATACCAAGCAGAACGCC	GGCGTTCTGCTTGGTATCGTCCTG
	2868	GCGTCTGTGATTCTGCCCTAACCC	GGTTAGGGCAGAATACAAGACGC
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	2870	TGTAAAGACCAGTGGCGGCTCTC	GAGAGCCGCCAAGTGGTCTTACA
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	2887	TCCACCTGTGTGCCTTATCCTCA	TGAGGATAAAGGCACACAGGTGGA
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	2889	TTGAGATTTTACGGTTCCCCGC	GCGGGGAAACCGTAAAAATCTCAA
	2890	CGATAGGACGTGGGCATGTCCCAG	CTGGGACATGCCACGTCTATCG
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	2892	TCACCGCAGCTAGAGTCGCGTTACC	GGTAACCGCAGCTCTAGCTGCGTGA
	2893	AGATAACGCCCACTGACGACATGC	GCATGTCGTAGTGGCGTTATCT
	2894	ACGCTTAGAGCTCCGATGCCGAAT	ATTCCGGCATCGGAGCTCTAACCGT
	2895	GGCGATAACTAAATTGTGCCGC	GCGGCACAATTAAAGTTATGCC
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	2898	TTCGAAATGTAATTCCCACGCGGA	TCCCGGTGGGAAGTACATTTCGAA
	2899	GCAGGGTTGGCTGTCTGTGGAGTC	GAATCCACAAAGACAGCCAACCTGC
	2900	CGTTGGTTGCTTCAAGAACCGGT	ACCGGTTCTGAAGCAACCAAACG
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	2903	GTGACGGTTGATTAACGACCGTGG	CCACGGTCGTTAATCAACCGTCAC
	2904	CTTATGGCAGCGCCAGGGCACTC	GAGTGCCTGGCGCTGCCATAAG
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	2907	TTCTTCATCAGCAGTCCCCGAGAA	TTCTCGGGACTGCTGATGAAGAA

	2908	AGTTGCGTCCCTGATGGCATT	AAAATGCCATCAAGGGACGCACT
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	2910	ACTTGGCCGGACGACAGCAAAGAC	GTCTTGCTGTGTCGGCCAAGT
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	2913	GCGCATAAGAAGGTCCGCTAAAGC	GCTTAGCGGACCTTCTTATGCGC
	2914	ACATCATCACGCCCTGGCGTGACCA	TGGTCACGCCAGGCGTGATGATGT
	2915	CCGGCGAAGTTGGTGTGATTAGA	TCTAATCACACCAAACCTCGCCGG
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	2918	CCTCTGGAGGGATTAGCCACGCT	AGCGTGGCTAATCCCCCTCCAGAGG
	2919	CAATAGCCATGTCACGGCAACGG	CCGTTGCCAGTGACATGGCTATTG
	2920	ACCCATGGTCCAACGTTCTTCG	CGAAAGAACGTTGGAACCATGGGT
15	2921	AATCTGGTCTGGCATCCTCCAAA	TTTGGAGGATGCCAAGACCAGATT
	2922	GTATACCGGTGCATGCTGAAGCAA	TTGCTTCAGCATGCACCGGTATAC
	2923	AGTGTCTGGTCGAGTCGACCCG	CGGGTCGACTCGAACCCAGAACACT
	2924	CGGGTATTCGACACACACGAGGGAC	GTCCTCGTGTGTCGAATACCCG
	2925	AGTGAACAGAGCGCTTGGTCACG	CGTGACCAAGCGCTGTGCACT
20	2926	TGCACCTATAGTTGGTGCCGGTG	CACCGGCACCAAACATAGGTGCA
	2927	TGCTCACGTACCAGGACACTCGAG	CTCGAGTGTCTGGTACGTGAGCA
	2928	AGTCCACACCTCGAACGACAGGCG	CGCCTGTCGTTGAGGTGTGGACT
	2929	CGCCGACCTGGTCAAAGAGCGCTA	TAGCGCTCTTGACCAGGTGGCG
	2930	GCCTAAGGGCCTGTCGTTCCGA	TCGGAAAACGACAGGCCCTAGGC
25	2931	TGTGCGTCTTATGTTCCGGTCTC	GAGACCGGAACATAAGCACGCACA
	2932	CAACC GTTGGCCGTAACAAAAATC	GATTTTTGTTACGGCCAACGGTTG
	2933	CGAGAATCAAGGCCTACCATCTCG	CGAGATGGTACGCCCTGATTCTCG
	2934	GCGTAGGCAGCCTCCAGGGAATGG	CCATTCCCTGGAGGCTGCCTACGC
	2935	GATGGTGTTCGCCAAGACCAAT	ATTGGTCTGGCGAAAACACCATC
30	2936	CAAGCTAGGGACAGAATTGCCAC	GTGGGCAATTCTGTCCCTAGCTTG
	2937	AAAATAGGC GAAACCGTTGTCGGC	GCCACGAA CGGTTGCCCTATTAA
	2938	TCAAGACCCGCAATGTGTTCATGT	ACATGAACACATTGCGGGTCTTGA
	2939	GCGGCTGGTAGACTCTTGACAA	TTGTGCAAAGAGTCTACCGCCGC
	2940	CAGGCCTAAACCTGAACCAAACGG	CCGTTGGTTCAAGGTTACGCCCTG
	2941	GCCGATCTGTGCTGAGGTCATCA	TGATGAACCTCAGCACAGATGGC
35	2942	GATATCGCGTCGCAATACCGCG	CGCGTGTATTGCGACGCGATATC
	2943	CCCTGCACGATTAAGCCACCTGTA	TACAGGTGGCTTAATCGTGCAGGG
	2944	TGACATACAGATTGTGTCGGCCC	GGGGCCACACAAATCTGTATGTCA
	2945	GTGGCGGCCGGTATTACGATGT	ACATCGTGAATACCGGCCGCAAAC
40	2946	TTTACCTGGCCATTGGTGAGCTC	GAGCTACCAATGGCCAGGTAAAA
	2947	CTCTACTCAATCAGGGTGGAGCG	CGCTCCCACCCCTGATTGAGTAGAG
	2948	GGGTTGGAGGGAGTCTGACCATT	AATGGTCAAGACTCCCTCCAACCC

	2949	CGAGGTCGGTAAGGAAAAGCTTC	GCAAGCTTTCTTACCGACCTCG
	2950	CTTACGCAGGCACCTCCGAGCTG	CAGCTGGAGGTGCCTGCGTAAG
5	2951	CATTGTATGCCACGTGATTGACG	CGTCAATCACGTGGCCATACAATG
	2952	GTACGGTGCGAGAGCGCCTAACG	CGCTTAGGCCTCTCGCACCGTAC
	2953	TTCCATATGCCGAAATGGACACAA	TTGTGTCCATTCGGCATATGGAA
	2954	TACGCCCTCCGCTATAGCTCGTA	TCACGAGCTATAGCGGAAGGCGTA
	2955	CTGTACGCCACGCATGAAGGGTGA	TCACCCCTCATGCGTGGCGTACAG
	2956	CTTACGCGTCCAATGACTGCCACC	GGTGGCAGTCATTGGACGCGTAAG
10	2957	CACATGGTAGAACTCGATGGCAG	CTGCCGATCGAGTTCTACCATGTG
	2958	CGCACCGGAAACTAGTGGATGTG	ACACATCCACTAGTTCCGGTGCG
	2959	ACTATGGCAACCGACACTGGTCC	GGACCAAAGTGTGGTTGCCATAGT
	2960	CTAGTTGCGCTACCCACCTGCAA	TTGCAGGTGGTAGCGCAAACTAG
	2961	TAGTATCGCCCGACAATAGCCTGG	CCAGGCTATTGTCGGCGATACTA
15	2962	CCAATATTCACGGCTGATCAGCG	CGCTGATCAGGCCGTAAATATTGG
	2963	ATGGCTATCCCTTACTGGCTCGCC	GGCGAGCCAGTAAGGGATAGCCAT
	2964	CAAAACTGGCAGGCTGGGACTT	AAGTCCCAGGCCTGCAAGTTTG
	2965	AATGACCGAGGCTGCAAGATTGAC	GTCAATCTTGCAGCCTCGGTATT
	2966	ATCATCTTCGCCACCAGACATGG	CCATGTCGGTGGCGAAAGATGAT
20	2967	CGTTATTACCGATGCACACGTTGC	GCAACGTGTGCATCGTAATAACG
	2968	CACACTGGCAATCGCCTCCCTCGT	ACGAGGGAGGCGATTGCCAGTGTG
	2969	AGGTTGGTAGGAAATCGGAGCGCT	AGCGCTCCGATTCCCTACCAACCT
	2970	GCTGAACCACTGTGGTCAAGATGC	GCATCTGACCACAGTGGTCAGC
	2971	CGTTGAGTACGACACGGTCGAGGT	ACCTCGACCGTGTGTAACGACG
25	2972	TTTTCCGCCGCAATGTGATCTAA	TTAGATCACATTGCGCGGAAAAA
	2973	ACAATACCTCGACCGCTCAGCATC	GATGCTGAGCGGTGAGGTATTGT
	2974	AGTATCCCTGCTGGCATAACCGGG	CCC GTGATGCCAGCAGGGATACT
	2975	TCTTGGGCTCGGTAGTTCACT	AGTGCTGAACCTACCGAGCCAAAGA
	2976	CCCTATATCGAGCCCATAAGGGCGA	TCGCCCTATGGGCTCGATATAGGG
30	2977	CACGAGTGGCATCAACGGCTACT	AGTAGGCCGTTGATGCCACTCGTG
	2978	TGCAGGGTCCGATGTGTTCAAGTA	TACTTGAACACATCGGACCCCTGCA
	2979	GCTTGACCGCTGCTAACCTCGTAC	GTACGAGGTTAGCAGCGGTCAAGC
	2980	TTTGCATCTCCACCATCCAGA	TCTGGATGGTGGAGAGATGCAAAA
	2981	AGAATGTGCACCGGCTTCCATCTT	AAGATGGAAGCCGGTGCACATTCT
35	2982	TGTTATGACCCGCTGTGGCGTG	CACGCCACAGAGCGGGTCATAACA
	2983	GGAGCTCTGTTCATCGAGGCTA	TAGCCTCGATGAAACAGGAGCTCC
	2984	CATTTGCTGTTGGGGTCCCAT	ATGGGACCCCCAACAGCAAAATG
	2985	CCCGCTCCTTCACGTGAGACGAGA	TCTCGTCTACGTGAAGGAGCGGG
	2986	GCGCTCAAGTCGATTGCCACAACC	GGTTGTGCAATCGACTTGAGCGC
40	2987	CGGTTGACGGAGACCGCAGTACTT	AAGTACTGCGGTCTCGTCAACCG
	2988	ACTCAAGACCGGTGCACCTCCAGC	GCTGGAGGTGCACCGGTCTTGAGT
	2989	TTCGTGTGCATGCAAGTAATGGC	GCCATTACTGCAACACGAAA

	2990	GCGGCGTTAGCTCGAGCTAACAAA	TTTGTTAGCTCGAGCTAACGCCGC
	2991	GGGTATCCTGCCCGAGCAGTAATT	AATTACTGCTCGGGCAGGATAACCC
	2992	GGCTCCGAATCTCTTGTCCGGTCT	AGACCGGACAAGAGATTGGAGCC
5	2993	AGGATGGCCACGCCGAATCAAAGT	ACTTTGATTGGCGTGGCCATCCT
	2994	GTGCGGGGACGTTACATAACGAG	CTCGTTATGAAACGTCCCCGCAC
	2995	ACTTTGACCTGAGGCCGTTGCA	TGCAAGCGGCCTCAGGTCAAAGT
	2996	ACTCCGCTTCATGGAGACC GTT G	CAACGGTCTCCATTGAAGCGGAGT
	2997	GATCGGAATTGCCGCATATTGA	TCAATATGGCGCGAATTCCGATC
10	2998	ATGCGTCCCCATGGAATGACTTT	AAAAGTCATTCCATGGCACGCAT
	2999	CCGCATCGCACGAAGGCAGGT CAT	ATGACCTGCCCTCGTGCATGCGG
	3000	CACCCATGCGTCTCCAATTCTG	CAGGAATTGGAGACGCATAGGGTG
	3001	TGATATGCATCGCTGAGCCTCTG	ACAGAGGCTCAGCGATGCATATCA
	3002	AGCTTCACACGCTACTGAACCTG	CAGGTTCA GTGAGCGTGTGAAGCT
15	3003	AACCCGGAACCTCCTCTCACTCGG	CCGAGTGAGAGGGAGGTTCCGGGTT
	3004	CTCGTCAA ACTTGGCCGAGGAGTC	GA CTCCTCGGCCAAGTTGACGAG
	3005	GTAGCTGGCAACAGGCAATCAGGA	TCCTGATTGCCCTGTTGCCAGCTAC
	3006	CTTGTCA CGGAATATTGCCAAGCG	CGCTTGGCGAATATTGTGACAAG
	3007	CAGTATCTGAAACACGGGGT GCTG	CAGCACCCGTGTTCA GATACTG
20	3008	GGCTAAAATGGCGCCACGTGTA	TACACGTGGCGCCCATTAGCC
	3009	ATGAGAGCCAAGCGCCTCACTCC	GGAGTTGAGGC GCTTGGCTCTCAT
	3010	TATTGTTAGGCACCGCTTCGCGCT	AGCGCGAAGCGGTGCCCTAACATA
	3011	GGA ACTAGATTGCCAGTGCTCGCC	GGCGAGCACTGGCAATCTAGTCC
	3012	AGTCGACCCCAAGGCAACTGGGTC	GACCCAGTTGCCCTGGGTCGACT
25	3013	GGTACTGTTAGCTCGACGATGCC	GGCCATCGTGAGCTAACAGTACC
	3014	CCGCAATACTTGACGGTAACAGGG	CCCTGTTACCGTCAAGTATTGCGG
	3015	AATTCCGGGTTGAA CGGTTGGAA	TTCCAACCGTTCAAACCCGGAATT
	3016	GACACGCAATCGGGTCTATGCGAA	TTCGCATAGACCCGATTGCGTGTC
	3017	GATTTGGCGTCTATTGCGTGAT	ATCACGCAATGAGACGCCAAATC
30	3018	TGCCATAGGGAGGAAACGCAATT A	TAATTGCGTTCCCTCCCTATGGCA
	3019	GAGGTGCCCATGTTAGTGGTGTCC	GGACACCACTAACATGGCACCTC
	3020	GCTTAGCGGTCTACGACCACCA	TGGTGGTGTATGACCGCTAAAGC
	3021	CCGCTACCAACAATCCGATTAACG	CGTTAATCGGATTGTTGGTAGCGG
	3022	GAGGA TCTGCCACATCGAGAAAG	CTTCTCGATGTGGCCAGATCCTC
	3023	CTCGTTGGTACCACGTTTGCCG	CGGCAAAACGTGGTACCAAACGAG
35	3024	AATACACGCGCGTAAACAGACGA	TCGTCTGTTACGCCGTGTATT
	3025	TGT CATGGCCAATGACAGTGGC	GCCACTGTCATTGGCCATGACA
	3026	ACAGCACTCCGACCCGTGTACGA	TCGTACACGGGT CGGAAGTGTGT
	3027	CTCCGTAAAGAGCACAGCTTGCC	GGCAAAGCTGTGCTCTTACGGAG
	3028	ACGAACAGGTAGGGATCGGTCTC	GAGGACCGATCCCTACCTGTTCGT
40	3029	TGGATCCACCTTACCGCGCCATCG	CGATGGCGCGGTAAAGTGGATCCA
	3030	AGTATCAAATAGCGGCCGGCAAG	CTTGCGCGCCGCTATTGATACT

	3031	GAATTACATTGTGGATGGAGGCCG	CCGCCTCCATCCACAATGTAATT
5	3032	CTCCTCGGGGAGTCGAGGAGTACG	CGTACTCCTCGACTCCCCGAGGAG
	3033	AGTGTGAGCCAACCTCCCACCAAT	ATTGGTGGGAGTTGGCTCGACACT
	3034	AAATGACATCCGTTGGCCACAGC	GCTGTGGCCAACGGATGTCATT
	3035	CGAATCATATGCCATCGAACTGG	CCAGTTCGATGGCGATATGATTG
	3036	TATAATGCACTCGCTGGTGCAGA	TGCGCACCAAGCGAGTGCATTATA
	3037	GCCAAGCAGATGGTAATTATGGCG	CGCCATAATTACCATCTGCTTGGC
10	3038	CACGCGGGAAAGAGCACGTAAGAAGT	AGTTCTACGTGCTTCCCAGCTG
	3039	TACCCGAGAATTGGAGAACAGCG	CGCTGTTCTCAAATTCTGGGTA
	3040	TGACGGCAAACGTGGCATCTATC	GATAGATGCCACAGTTGCCGTCA
	3041	CACAGTGTCCAGCCCTGACGAT	ATCGTCAAGGGCTGGAACACTGTG
	3042	TACCCGCCACACATGAAAGTTGG	CCAACTTCATGTGTGGCGGGTA
	3043	TGGCATATTAAAGATTGGCGACG	CGTCGCCGAATCTAAATATGCCA
15	3044	ACTGAAAAAAAGAACGGTAGCGGG	CCCGCTACCCGTTCTTTTCAGT
	3045	TCTGACCGCAATAGGTGGTATTG	CAATGACCACCTATTGGGTCAAGA
	3046	ACTTTTGCGGGCCCTCTCTCGT	ACGAGAGAGGGCCCGCCAAAAGT
	3047	CTGCCAGATCATTGGCGATCCG	CGGATCGCGCAATGATCTGGCAG
	3048	CGGAGGTTAAATGCTTAACCGGC	GCCGGTTAAAGCATTAAACCTCCG
20	3049	AGGCGTCTCCAAACGTCTTCTGT	ACAGAAGGACGTTGGAGACGCCT
	3050	AGATGCTATCCTGAGTGGCCTGC	GCAGGGCCACTCAGGATAGCATCT
	3051	ACAGGGTGAAGAGACCGTGGGATG	CATCCCACGGTCTCTCACCTGT
	3052	GAATGCTAACGGACGACACGACG	CGTCGTGTCGTCCGTTAGACAGTC
	3053	AGCTGTTAGGACCCGACAACCGGT	ACCGGTTGTCGGGTCTAACAGCT
25	3054	TTGCGTAGTGTGGCATTCTCT	AGAGGAAATGCCACACTACGCAA
	3055	ATGCGCGCTTCTTCCTTGATGTA	TACATCAAGGAAAGAAGCGCGCAT
	3056	TTAAGGGCGTCCCGCTTATTCAG	CTGAATAGACGCGGACGCCCTAA
	3057	ACCTTAAACTGTACCGCGGCC	GGGCCGCGGTACAAGTTAAAGGT
	3058	AGGGATGCAGAGGCACCATGTT	AACATGTGGTGCCTCTGCATCCCT
30	3059	CGGTTGACGTATGAGCATCCGCA	TGGGGATGCTCATACGTCGAACCG
	3060	CAGGGCGATAGTCACATGGAGGTT	AACCTCCATGTGACTATGCCCTG
	3061	GCTTGACTGCCCGTTCATATGT	ACATATGAAACGGGGCAGTCAGC
	3062	CGAAGGGGTTGTGCAATTACCGA	TGGGGTAATTGACAACCCCTCG
	3063	AAAACGCACCGCAATGACAAAATT	AATTTTGTCAATTGCGGTGCGTTT
35	3064	ATTCCTGGACAAGACCCCTAACCG	CGGTTGAGGGTCTGTCCAGGAAT
	3065	CCTACCTGCCTGCTAGCGGTGAGG	CCTCACCGCTAGCAGGCAGGTAGG
	3066	GCTCGTAAATGGGGAGGAATTGGA	TCCAATTCCCTCCCCATTACGAGC
	3067	ACATGAAAACAGGCTAACGGGG	CCCCAATTGAGCCTGTTTCATGT
	3068	GTTCCGCACATGGATTGAGGTCTC	GAGACCTCAATCCATGTGCCAAC
40	3069	GGCACCCAAATACCACGAAGAAGAA	TTCTTCTCGTGGTATTGGGTGCC
	3070	AGGGGCATTGCAACTCCATCTT	AAAGATGGAGTCGAAATGCCCT
	3071	CATCATCACAAAGGAACGTCGGTG	CACCGACGTTCTTGTGATGATG

	3072	TAAGACCCACCGTCAGCAGCAGC	GCTGCTGCTGACGGTGGTCTTA
5	3073	CCCCAGCGTAATGCACCACATAG	CTATGTGGTGCATTACGCCCTGGG
	3074	GCAGGTCGAACGCTAGTGGTGAA	TTCAACCACTAGCGTTCGACCTGC
	3075	GGAACTTAGGAGTTACGTCGCCA	TGGCGACGTGAACCTCTAAGTCC
	3076	GCAGATAACGGCTAGCTGAGGTGGC	GCCACCTCAGCTAGCCGTATCTGC
	3077	CACAGGCCTAGAGCCTCGCGTTC	GAACGCCGAGGCTCTAGGCCTGTG
	3078	TTTTGCGCGCATGAGGTTCTTA	TAATGAACCTCATGCGCGAAAAC
10	3079	TTGCGCCTGATGCCAGCAGTACTA	TAGTACTGCTGGCATCAGGCGCAA
	3080	GATATCAGGCTTCCCCTGCGC	GCGGCAGTGGAAAGCCTGATATC
	3081	TGCGCGGAGACGGAGATCTATGAA	TTCATAGATCTCCGTCCTCGCGCA
	3082	CATTGGTGGCTGAGAGTGGAC	GTCCACTCTCAGCCAACACCAATG
	3083	GTCGGCACTGGGACCACTTAATA	TATTAATGGTCCCCAAGTGCCGAC
	3084	ATCGATCGGTGTCACACGGAG	CTCCGTGGTGAGACACCGATCGAT
15	3085	CGTAGCCTCCACCGTGTGATAG	CTATCGACACGGTGGAAAGGCTACG
	3086	CGCTCTCCGCTGAGGAAAGGGG	CCCCTTTCTCAGACGGAGAGCG
	3087	TCGCCCCAGCCAAGGGATATATTGC	GCAATATATCCTGGCTGGGGCGA
	3088	TCTCTTGCAAGGAACCTGCCGTC	GACGGCAGAGTTCTTGCAAGAGA
	3089	GTCCTGGACAGACGGAGGGTGTAA	TAACACCCCTCCGTCGTCCAGGAC
20	3090	GCCAAATTAAAGCGGGCTGTAATC	GATTACGAGCCCGCTTAATTGGC
	3091	CCATTGTTGACCGATGGGAGGGG	CCCCTCCCCTCGGTCAACAAATGG
	3092	TGGTAAAAGAGCACGATCCAGGA	TCCTGGATCGTGTCTTTGACCA
	3093	CGCTACTAACGACGCCCTGTCCAC	GTGGACAGGGCGTCTAGTAGCG
	3094	CATACCTCCCCTGGATTCACTG	CAGTGAATCCAAGCAGGGAGGTATG
25	3095	CCGCGGAAGGAATGTCATCTACAA	TTGTAGATGACATTCTCCCGCGG
	3096	CACGGGACATTCAATTACAGGACG	CGTCCTGTGAATGAATGTCCCCTG
	3097	AGGAGTCACCCACTCCGCACAAAA	TTTGTGGGAGTGGGTGACTCCT
	3098	TCATGACAGCGCACCCATACCAT	ATGGTATGGGTGCGCTGTCA
	3099	GGTAGGGGACTATCGATCGTGTG	CAGCACGATCGATAGTCCCCTACC
30	3100	ATGTCTCACTACCGCACGTAGCGG	CCGCTACGTGCGGTAGTGAGACAT
	3101	ACGGAGGAGCGACTCGTCGCTGC	GCAGCGAACGAGTCGCTCCCTCGT
	3102	GAAGTCTGCGCCGGTGGACGGAC	GTCCGTCCACCGGCGACAGACTTC
	3103	CCGTAACGTATTCCGACGAGCG	CGCTCGTCCGAATACACGTTACGG
	3104	CGTGGAAAGCGACTAACCAATCGT	ACGATTGGTTAAGTCGCTTCCACG
	3105	GGCATGGCTATGCCCTCACACTAG	CTAGTGTGAGGCATAGCCCATGCC
35	3106	GGGTGTTACCGTACGTCGTT	ACGAACGATGCTGAAATACGACCC
	3107	AATGGTCGCGCAAACCGTAAGAAT	ATTCTTACGGTTGCGCGACCATT
	3108	CTGGATTGGTACGTCACGTTT	AAACGTTGACGTACCGAATCCAG
	3109	CGCAAAACACCCGTAGCCAAGAA	TTCTGGCTACGGGTGTTTGCG
	3110	TATGGATACGCTTGGACTGGC	GCCCAGTCAAAGCGTATCCATA
40	3111	GCTTCAAACCGCCTCACGCTGGT	ACCAGCGTGAAGCGCGTTGAAGC
	3112	TACAGCCCGCTTACCTGCCACC	GGTGGCGAGGTAGAGCGGGCTGTA

	3113	TCAACCGATGTCAAATGCACGTT	AACGTGCATTTGACATCGGTTGA
5	3114	AGCTCTCTCCGAAGTAGGGCGGTA	TACCGCCCTACTTCGGAGAGAGCT
	3115	ACGCACACATGGAGACTTGGCTCC	GGAGCCAAGTCTCATGTGTGCGT
	3116	TTCTTGAAAGCTAGTGGGCGCTA	TAGCGCCCCACTAGCTTCAAGAA
	3117	CAATCACGGCTGGCTATTCTGTG	CACAGAATAGCCCAGCCGTATTG
	3118	GTGGCGACCCGTGGTAAAGAGT	ACTCTTACCCGACGGGTCGCCAC
	3119	CGTCGAATGCCGAACCAGTTAAGT	ACTTAACGGTTCGGCATTGACG
10	3120	TGCGTATTCGATGCTCACAGCTG	CAGCTGTGAGCATGCAAATACGCA
	3121	CGCAGTTGGTTGTGACGGCTGC	GCAGCCGTGCACAAACCAACTGCG
	3122	GTTTTCCGTGAAAATGGCATCG	CGATGCCAGTTTACGGAAAAAC
	3123	ACAGGTTCCCTCACCAACGATTGA	TCAAATCGTGGTGGAGGAACCTGT
	3124	CTAGCGCGCTTTAGGTCCCTGCG	CGCAAGGACCTAAAAGCGCGCTAG
	3125	CAAAATCAAAGGGATCAACGGGT	CACCGGTTGATCCCTTGTATTG
15	3126	AACGTAACCCCAGTGAGTCAGGCA	TGCCCTGACTCACTGGGTTACGTT
	3127	TCAACCGGTGCACTTAAACGCC	GGCGTTCTAAAGTGCACCGGTTGA
	3128	ATCGCAAAGTTGCAGCGAATACT	AGTATTGCCTGCAACTTGCAT
	3129	ATATGTCCTGGTGCTGCACAAC	GTTGTGCAGCACCCAGGGACATAT
	3130	TGGCACTTTGTAGTGCCTGGTGG	CCACCGCAGCACTACAAAGTCCA
20	3131	ACGCACGACGTCTTAAGCTCG	CGAGCTTAGAAGGACGTCGTGCGT
	3132	CCCACGTGCACTATAAGGATTTCG	CGAAATCCCTATAGTCACGTGGG
	3133	CCCGCGCTTGGTCAGTCATCCTTC	GCAAGGATGACTGACCAAGCGCGG
	3134	AGCGGCTCAGGGATAACAACAGG	CCTGTTGTTATTCCCTGAGCCGCT
	3135	ACAACCGCATCGGAGGCAACCGT	ACTGGTTGCCTCCGATCGCGTTGT
25	3136	AGCAATTGCCTCCGTAGAAACCCA	TGGGTTCTACGGAGGCAATTGCT
	3137	GAGTCGTGGCATGCCCTGCTATCG	CGATAGCAGGCGATGCCACGACTC
	3138	TCTATGCAAATACTGCGCTTGC	TCGCAAGCCAGTATTGATAGA
	3139	TCAGCTTAAGTTACGGTGTGGCG	CGGCCACACCGTAACCTAAGCTGA
	3140	TCCAAGGTGAAACAGGGATCAGAA	TTCTGATCCCTGTTGACCTTGGA
	3141	GTTAGGCTGGCGTCAATAGCGCT	AAGCGCTATTGACGCCAGCCTAAC
30	3142	GGTGTATAAGGAAGAGGGCATCG	CGATGCCCTCTTCCTTATGACACC
	3143	CCGGCGGGCTAGATCAATATTCT	AGAAATATTGATCTAGCCCAGCGG
	3144	CTAACGTCAAGTTACGCCCCGA	TGGGGCGTAAACCTGACGTTAG
	3145	GCAGCACAGTTCCGATTGCGG	CCGAAATCGGAAACTGTGCTGC
	3146	CGCACGCAAGGGAGGGATGACTG	CAGTCATCCCTCCCTGCGTGC
35	3147	CGGGGCCGAAAAGGACGTACAAG	CTTGTGACGTCTTTCGGCCCCG
	3148	TTCTCCAACACGGCTAACCGGTAG	CTACCGGTTAGCCGTGTTGGAGAA
	3149	TTACAGCCTGGCCCGAGGTAGTTG	CAACTACCTCGGGCCAGGCTGTAA
	3150	TTTCGGGCAGCATGAGTTATCGAA	TTCGATAACTCATGCTGCCGAAA
	3151	CTACTGGACGCCCTGCTCGAAGT	ACTTCGAAGCAGGGCGTCCAGTAG
40	3152	GGTCGTCCGACGTGAAAAGACAA	TTGGTCTTTCACGTGGACGACC
	3153	GTTTTCGAGCTTTCTCCGCAGG	CCTGCGGAGAAAGAGCTCGAAAAC

	3154	GCGTGAAGGTACCCAGTGTACAG	CTGTGACACTGGGTACCTCACGC
5	3155	TTTCTGAACGCTTCGACGCAACAC	GTGTTGCGTCGAAGCGTTCAGAAA
	3156	TGCTAATAAGCACGCCAGCCCGT	ACGGGCTAGGCGTGCTTATTAGCA
	3157	AAATTAATTGTGGTGGCTCCGGCG	CGCCGGAGGCCACCACAATTAAATT
	3158	TTACAATCCTCGGGCTCACTGACA	TGTCAGTGAGCCCAGGATTGTA
	3159	GCTGAAGGACAAGGCGTGGGCAAC	GTTGCCACGCCCTGTCCTTCAGC
	3160	GGGATAGGAGAACCTCGCAATGGT	ACCATTGCGAGGGTCTCCTATCCC
	3161	TTGCAGTACGTCCCTGCGCATGAA	TTCATGCGCAAGGACGTACTGCAA
	3162	TTGATCACTGGATTGGGTGCGAAC	GTTCGACCCAATCCAGTGATCAA
10	3163	TCTGCAGACGTTGCGAGAGATGAT	ATCATCTCTCGCAACGTCTGCAGA
	3164	AGTCTAGCAGGGATCGAACGCGGAT	ATCCGCTTCGATCCCTGCTAGACT
	3165	GGGGTCCCCAACAACTAATGAAG	CTTCATTAGTTGTTGGGGACCCC
	3166	CAACCTCTTATGTGGTGTGCGCA	TCGCGCACACCACATAAGAGGTTG
	3167	CTCGCTGGGTTGCTGGAGTAGCAC	GTGCTACTCCAGCAACCCAGCGAG
15	3168	CGTTGTATTGTCAACGCGAAGTT	AACCTCGCGTTGCACAATACAACG
	3169	GGGCTCAAAGTGCCTGAGTCGAAA	TTTCGACTCAGGCACITTGAGCCC
	3170	CTGCTGTGCCCTCTCAGTGAGAGC	GCTCTCACTGAGAGGGCACAGCAG
	3171	CGGACGTACTGTTGGAGTCCTCA	TGAGGACTCCGAACAGTACGTCCG
	3172	GTATACCACCATACCGGGACCGCA	TGGGTCCCGGTATGGTGGTATAC

TABLE 3

Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
17	TTCCGCCGTGCGTAGGCTTTCAA	TTGAAAAGCCTACACGGACGGCGAA
18	GTTCCCAGTGAAGCTGCGATCTGG	CCAGATCGCAGCTTCACTGGGAAC
19	TACTTGGCATGGAATCCCTTACGC	GCGTAAGGGATTCCATGCCAAGTA
20	ACTAGCATATTTCAGGGCACCGGC	GCCGGTGCCCTGAAATATGCTAGT
21	GAACGGTCAATGAACCCGCTGTGA	TCACAGCAGGGTTCATTGACCGTTC
22	GCGGCCTGGTTCAATATGAATCG	CGATTCATATTGAACCAAGGCCGC
23	GATCGTTAGAGGGACCTTGCCCGA	TCGGGCAAGGTCCCTTAACGATC
24	TGGACCTAGTCCGGCAGTGACGAA	TCGTCACTGCCGGACTAGGTCCA
25	ATAAACTACCCAGGACGGCGGAA	TTCCGCCCGTCTGGTAGTTTAT
26	CATCGGTTCGCGCCAATCCAGATA	TATCTGGATTGGCGCGAACCGATG
27	GTCCCCATAGAGCCGACCACCC	AGGGTGGTCGGCTATGCCCGAC
28	CTTGGGTATGATTACCGTGCTA	TAGCACGGTGAATCATGACCCAAG
29	TGCCTAACGTGCTAATCAGCAGCG	CGCTGCTGATTAGCACGTTAGGCA
30	CGCATGTTGGAGCATATGCCCTGA	TCAGGGCATATGCTCCAACATGCG
31	AGCCACTGCATCAGTGCTGTTCAA	TTGAACAGCACTGATGCAGTGGCT
32	GGTTGTTTGAGGCGTCCCACACT	AGTGTGGACGCCCTAAACAAACC
33	TCGACCAAGAGCAAGGGCGGACCA	TGGTCCGCCCTTGCTTTGGTCGA
34	GACATCGTATTGCGCATGGATCA	TGATCCATGCGCAATAGCGATGTC
35	GAAATACGAAGTCTGCGGGAGTCG	CGACTCCCCCAGACTTCGTATTC
36	TGTATGAATGATTGATCGCGCA	TCGCGCGATCAATCATTGACAA
37	ATATCGGGATTGTTCCCGGTGAA	TTCACCGGGAACGAATCCCGATAT
38	GCGAGCGTACCGAACGGGCCTAGAA	TTCTAGGCCCTCGGTACGCTCGC
39	TTACCGGCAGCGGACTCCGAATT	AATTCGGAAGTCCGCTGCCGGTAA
40	GTAATCGAGAGCTGCGCGCCGTCT	AGACGGCGCGAGCTCTGATTAC
41	CCTGTTAGCGTAGGGCAGTCGATC	GATCGACTGCCCTACGCTAACAGG
42	TAGCGGACCGGCAGAATGAGTTCC	GGAACTCATTGCGGTCCGCTA
43	GGTACATGCACTACCGCGACTCGG	CCGAGTGCCTAGTGCATGTACC
44	AATTATCTCGGACTCCGCGGT	TACCGCGGGAGTCCGAGATGAATT
45	GCCAAATCTGGATTGGCAGGAATG	CATTCCGCCAATCCAGATTGGC
46	TGCATTTCCGGTTGAGGCACATCC	GGATGTGCCTCAACCGAAAATGCA
47	CCGCTCAATTACCATGCTTCGCT	AGCGAACGATGGTAATTGAGCGG
48	CTCGGAAAGGTGCAACTTGGTGT	ACACCAAAGTTGCACCTTCCGAG
49	AATTGACCAAGCAGAACGTCCC	ATGGGACGTTCTGCTGGTCAATT
50	GCCAGAGTCTCAACCTCACGGGAT	ATCCCCTGAGGTTGAGACTCTGGC
51	CCAACAACGGAACGGGACCCGC	GGGGGTTCCCGTTCCAGTTGG
52	GAGAACTGATCGCTGAGGGGCATG	CATGCCCTCAGCGATCAGTTCTC
53	GGCACACTAGACTTGTGGCACCGA	TCGGTGCCACAAGTCTAGTGTGCC

	54	TCACATCCAATATGGTCCCGGAA	TTCGCGGACCATAATTGGATGTGA
	55	GTCCTGCCGGTGTGACCGCTTCATT	AATGAAGCGGTACACCCGGCAGAC
	56	CATCGCAGAGCATAAACACCCCTCA	TGAGGGTGTTATGCTCTGCGATG
5	57	GTTGGTATCTATGGCAGAGGCCGA	TCCGCCTCTGCCATAGATACCAAC
	58	ACGAGGTGCCGCTGAGGTTCCATT	AATGGAACCTCAGCGGCACCTCGT
	59	GGAATGAGTGGACCCAGGCACATT	AATGTGCCTGGGTCCACTCATTC
	60	TGTCAATATGCGTCCGTGTCGTC	AGACGACACGGACGCATATTGACA
	61	TGATGAGCCTCAGGGTACGAGGCA	TGCCTCGTACCCCTGAGGCTCATCA
	62	CACCGCGGTGTTCCCTACAGAATGA	TCATTCTGTAGGAACACCGCGGTG
10	63	TTGTTGCCAATGGTGTCCGCTCGG	CCGAGCGGACACCATTGGCAACAA
	64	TTAACCTGCGTCTGCCCTTTCCT	AGGAAAGGGGCAGACGCAGGTTAA
	65	AGGC CGGT CCTGCC TAGTGACG	CGTCACTAAGGCAGGAACGCCCT
	66	TAGGGCGATGGCACGAAGCTCAA	TTGAAGCTTGTGCCATGCCCTA
	67	TGCATAGAGCCAAAGTCGGCGATG	CATGCCGACTTGGCTATGCA
15	68	TTGAGAGGCAGGTGGCACACCGGA	CCCGTGTGCCACCTGCCCTCAA
	69	TCCGCATTGTGAGAAAAAACGAGC	GCTCGTTTTCTCACAATGCDDA
	70	GGCGGTTCCGTAGCTATAGGTGC	GCACCTATAGCTACGGAAACGCC
	71	GGTAAAATTCGTAGCCACGGGC	GCCCGTGGCTACGAAATTTCACC
	72	CCGACGGAGGATGAAGACAATCAC	GTGATTGTTCATCCTCCGTGG
20	73	CCAGTTGCCCAATTGCCAAA	TTTGGCGAATTGGGCCAAACTGG
	74	GGATCTATTAGGCCGTGCGCACAG	CTGTGCGCACGGCTAATAGATCC
	75	CGGATGTCAACGTTGGACTTCA	TGAAAGTCAAACGGTGACATCCG
	76	ATCGCAAATCCTGCTCGTCCCTAA	TTAGGGACGAGCAGGATTGCGAT
	77	CAGGGCATGCAATAATCGAGGTT	GAACCTCGATTATTGCATGCCCTG
25	78	CATGCGTTGATATATGGGCCAAG	CTTGGGCCATATATCAACGCATG
	79	CAGCTGCAGCTTGTGACCAACCAC	GTGGTTGGTCACAAGCTGCAGCTG
	80	TTGTATGCTGCCGACCGGGGACC	GGTCGCCGGTCGGCAGACATAAC
	81	GATGGCGCCGTTGATAGGTATGG	CCATACCTATCAACGGCGCCATC
	82	ATGAGAATGCCGGCAATCTGCTA	TAGCAGATTGCCGGGATTCTCAT
30	83	ATTTGCACTGACCGCAGGCTCGTG	CACGAGCCTCGGGTCAGTGAAAT
	84	CAGGGAGAACGGTTAACGTTCCC	ACGGGAACCTAACGGTTCTCCCTG
	85	AGGCCGGCGATCGAGGAGTTGGT	ACCAAACCTCTCGATGCCGGCCT
	86	ACACGGTGGTCTCTGATAGCGACC	GGTCGCTATCAGAGACCACCGTGT
	87	GTGCAACGCCGAGGACTCCATCA	TGATGGAAGTCCTGGCGTTGCAC
35	88	TCGGTGCTGTAGCCATTCCGAT	ATCGGAATGGCTATCAGGCACCGA
	89	TGAAATACCAACACAGCCAATTGGC	GCCAATTGGCTGTGTGGTATTCA
	90	GCATCGTGTACATGACTGCCCGA	TCGCGGCAGTCATGTACACGATGC
	91	CAGTGTCTAACGGCGCGTGAA	TTACGCGCGCCGTTAGAACACTG
	92	CGCTTGCAACGTTGCACCTACTCT	AGAGTAGGTGCAACGTTGCAAGCG
40	93	CGAAAAACTAGTGGCTGCCCGCG	CGCGGCGAGCCACTAGTTTCG
	94	CTTCAGGGAACTGCCGGAGTCG	CGACTCCGGCAGTCCCTGAAAG

	95	TTGTGGCCTTCTGTAAAGGCACG	CGTGCCTTACAAGAAGGCCACAA
	96	TCCACGAACGGCGACCGCTGTCT	AGACAAACGGGTCGCCGTGGA
	97	CGACCTTGCACGAAACCTAACGAG	CTCGTTAGGTTCTGTCAAGGTCG
5	98	GTGCAGCTTCACGAGCCAGCCTGA	TCAGGCTGGCTCGTAAGCTGCAC
	99	CGCTTCTGTGCGAATAGACGATGA	TCATCGTCTATTGACGAAAGCG
	100	TGCGCTTACAGGCTCCTAGGGTC	GACCACTAGGAGCCTGTAAGCGCA
	101	CACCGCCTAGTCGCGATCGCATA	TATGCGATCGCGACTAACGCGTG
	102	CGGAGGGAGGGAGCTAGCCTCGA	TCGAAGGCTAGCTCCCTCCCTCCG
10	103	GCATCCGGCCTGTTGATGACGCCT	AGGCCTCATCAACAGGCCGGATGC
	104	AGGCCAATCGATCTTATTGCCGAG	CTCGGCAATAAGATCGATTGGCCT
	105	CCTTCCAATGATTGCGATACGCCCA	TGGCGTAGCAGCAATCATTGGAAGG
	106	AACACTTGATCAGGGGGTCGTCT	AGACGACCCGCGCTGATCAAGTGT
	107	TGGAATCAAGGCCGTAAGGACAG	CTGTCCTTACGGCCTTGATTCCA
	108	GCTCCCGTAACCTGTCCACCAGTG	CACTGGTGGACAGGTTACGGGAGC
15	109	AGTGGTGAATGGCCGCTACCGTGA	TCAGGGTAGCGGCCATTACCACT
	110	TGTTGAAGCGAGCTAAAACGGCCA	TGGCCGTTTAGCTCGCTTCAACA
	111	CAGCGCTCCAGAATTGACAGCAAT	ATTGCTGTCAATTCTGGAGCGCTG
	2	TTCGAAGCGCACGTCCTTCAA	TTGAAAAGGGACGTGCGCTTCGAA
	3	AACCGTGGGAATGGGACATCAA	TTGATGTCCCATTCCCCACGCGTT
20	114	CACGAGATACCGGGCGTAAGGGTGG	CCACCCCTACGCCGGTATCTCGTG
	115	CTACGGCAAACGTGGAATGGGT	ACCCATTCCACACGTTGCCGTAG
	116	GTAAGGGCGATGACGGGCGAACTAC	GTAGTTCGCCGTACGCCCTAC
	117	AATCGACCTCCGCACACATTGCA	TGCGAATGTGTGCGGGAGGTGCGATT
	118	GAGTCAGCATGGCGGCGGAGATT	GAATCTCCGCCGCATGCTGACTC
25	119	AGATAAAGACGCTGGCAACACGGG	CCCGTGTGCGCAGCGTCTTATCT
	120	GGTACCTCAACCGGAACCACTGT	ACAAGTGGTTCGCGTTGAGGTACC
	121	AAGCGATGGCTACCCAAGAGCGAT	ATCGCTCTGGGTAGCCATCGCTT
	122	AGAGCTTATGCAGAACCGAGCGCC	GGCGCCTGGTTCTGCGATAAGCTCT
	123	ATCGGTCTCACCGAGGTTGGATA	TATCCAACCCCTGCGTGAGACCGAT
30	124	TAGGTTGCCGCCAGAAGAACAT	ATGTTCTCTGGCGGGCAACCTA
	125	CGGTGCTGGCAAAAGCCTGTAG	CTACAGGCTTGTGCAACAGCACCG
	126	TGATGAAAGTTGGCGGAGGACAC	GTGTCCCTGCCGAAACTTTCATCA
	127	GTTGAGTGCAGGATGCAGCGATAG	CTATCGCTGCATCCTGCACTCAAC
	128	AACATTGCGCGGTCCACCAAGGGTT	AACCCGGTGGACCGCGCAATGTT
35	129	GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCC
	130	TCGAGCTGGTCCCCGTGACGTGT	ACACGTTCACGGGGACAGCTCGA
	131	GTCTTGGGGCCGCTTAGTAAAA	TTTCACTAAGCGGCCCAAGAC
	132	ACTGTTGGCTGCTCTCATGTCCA	TGGACATGAGAGCAAGCCAACAGT
	133	AGGACCATTGGAAAGCGAAGATA	TATCTCGCCTCCGAATGGTCT
40	134	CTTGGGAGGCATCCGCTATAAGGA	TCCTTATAGCGGATGCCCTCCAAAG
	135	AATAAACGGAACGCACCGCTACAG	CTGTAGCGGTGCGTTCCGTTATT

	136	TTGTACGTGCGGTCCCCATAAGCA	TGCTTATGGGGACCGCACGTACAA
	137	CGCACCAAACGTAGTTCCCAAGAC	GTCTGGAAACTCAGTTGGTGCG
	138	ACCTGATCGTCCCCATTGGGAA	TTCCCAATAGGGGAACGATCAGGT
	139	GGAACAGAGGCAGGGGACTGAGC	GCTCAGTCCCCTGCCCTGTTC
5	140	CCCTGCCTTGGCGTGTGGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
	141	ACTCTGACACGCCAACCTCCGGAAG	CTTCCGGAGTTGGCGTGTCAAGGT
	142	CTGACGGTTTCATTGGCGTGCC	GGCACGCCGAATGAAAACCGTCAG
	143	TGCGGTGGTTCATGGAGCTGGCC	GGCCAGCTCCAATGAACCACCGCA
	144	GCATGGCCAACTAGTGACTCGCAA	TTGCGAGTCACTAGTTGCCATGC
10	145	AGGCCGTAAGCGAATCTCACCTG	CAGGTGAGATTGCTTACGGCCT
	146	CGAATATTATGCCGAGAACCGCG	CGCGGATTCTCGGCATAATATTG
	147	ACAGACGAGCTCCCAACCACATGA	TCATGTGGTTGGGAGCTCGTCTGT
	148	GGACGGTTGTGCTGGATTGTCTG	CAGACAATCCAGCACAACCGTCC
	149	AAAGGCTATTGAGTTGGTGGCG	CGCCCAACCAACTCAATAGCCTT
15	150	GATGGCCTATTCGGAGATCGGGCC	GGCCCGATCTCCGAATAGGCCATC
	151	GATCCAGTAGGCAGCTTCATCCCA	TGGGATGAAGCTGCCTACTGGATC
	152	AATAACTCGCGCGGGTATGCTTCT	AGAAGCATACCCGCGCAGTTATT
	153	GGAGGAGGTTGTCTCGGAAAGCA	TGCTTCCGAGACAAACCTCCTCC
	154	CTTGGTATGGCACATGCTGCCG	CGGGCAGCATGTGCCATACCAAAG
20	155	AGAAAGGCTCGAGCAACGGGAACT	AGTCCCCTGCTCGAGCCTTCT
	156	AATCTACCGCACTGGTCCGCAAGT	ACTTGCAGGACCAGTGGTAGATT
	157	CGTGGCGGCCACAGTTTGAGG	CCTCCAAAAACTGTGGCCGCCACG
	158	TTGCAGTTCAATCCATACGACGT	ACGTGCGTATGGATTGAACTGCAA
	159	GGCCCAAAGCCCCAGACCATTAA	TAAAATGGCTGGGGCTTGGGCC
25	160	CGCCTGTCTTGTCTCCGGACAAT	ATTGTCCGGAGACAAAGACAGGCG
	161	TGAGGCAACAGGGGCCAAAAACTA	TAGTTTGGCCCTGTTGCCCTCA
	162	AGCGGAAGTAGTCCTCGGCTCGTC	GACGAGCCGAGGACTACTCCGCT
	163	GGCCCCAAGGCTTAGAGATAGTGG	CCACTATCTCTAACGCCCTGGGGCC
	164	GCACGTGAAGTTAACCGCGATTC	GAATCGCGTTAAACCTCACGTGC
30	165	AGCGGCAGAACGTTCTTGACGG	CCGTCAAGGAACGTTCTGCCGCT
	166	TCGTCGAGCAGACGAGATTGACG	CGTCAATCTCGTCTGCTCGACGA
	167	TCTTGCCCGTAACTGACTGCTT	AAGCAGTCAGTACGCCGAAAGA
	168	TTTATGTGCCAAGGGGTTAACCGA	TCGGTTAACCCCTGGCACATAAA
	169	TGTTACTGTGGTTACGGCAGTCC	GGACTGCCGTGAACCACAGTAACA
35	170	CGCGCCTCGCTAGACCTTTATTG	CAATAAAAGGTCTAGCGAGGCGCG
	171	ACAAATGCGTGAGAGCTCCAACT	AGTTGGGAGCTCTCACGCATTGT
	172	CGCGCAGATTATAGACCCGAATGT	ACATTGGGTCTATAATCTGCGCG
	173	CAAATAACGCCGCTAACCGGT	ACGCCGATTAGCGGGCTTATTG
	174	CCTTCGTGCATCGGTGATGATGTT	AACATCATACCGATGCACGAAGG
40	175	TGAACACGAGCAACACTCCAACGC	GCGTTGGAGTGTGCTCGTGTCA
	176	CAGCAGATCCTCGTAGCGGCGT	ACGACCGCTACGAAGGATCTGCTG

	177	GGAACCTGGTAGTTGCGCTCAT	ATGAGGCACAACTCACCAGGTTCC
5	178	TCATAAGCGACAATCGCGGGCTTA	TAAGCCCGCGATTGTCGCTTATGA
	179	CCCAACGTCACTGAAGCTCACAGT	ACTGTGAGCTTCAGTGACGTTGGG
	180	TGTCAGAGCCCAGCAGACGG	CCGCTGAGTCGCGGGCTCTGACA
	181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
	182	CTCAGAAGTCTCGCGAAGTGGG	CCCAGTTGCCGAGGACTCTGAG
	183	ATCCTTTATCTACTCCGCGCGA	TCGCCGCGGAGTAGATAAAAGGAT
10	184	AGGCGTGAGCAACAGGATAAACCC	GGTTTATCCTGTTGCTGCACGCCT
	185	ACTCTCGAGGGAGTCTCTGGCACA	TGTGCCAGAGACTCCCTCGAGAGT
	186	TTGCCAGGTCCATCGAGACCTGTT	AACAGGTCTCGATGGACCTGGCAA
	187	TCCACTATAACTGCCGGTCCGTGT	ACACGGACCCGAGTTATAGTGGA
	188	GCCCAGTCGGCTCTAACAGTCG	CGAACTTGTAGAGCCGACTGGC
	189	CGGAACGGATAATCGCGTCAGGT	ACCTGACGCCGATTATCCGTTCCG
15	190	TAAAATAAGCGCTGGCGGGAGGA	TCCTCCGCCAGGCCCTTATTITA
	191	GCGCACTCGTAAACCTTCTCGC	GCGAGAAAGGTTTACGAGTGC
	192	AGTTTGCCAGGTACTGGCAAGTGC	GCACTTGCCAGTACCTGGCAAAC
	193	ACAACGAGGGATGTCCAGCGGCAT	ATGCCGCTGGACATCCCTCGTTGT
	194	TTCGCAGCACCGCTAGGTACAGT	ACTGTACCTAGCGGGTGC
20	195	TAACCCGATTTTGCAGTCTGCC	GGCAGAGTCGCAAAATCGGGTTA
	196	CGTCGCATTGCAAGCGTAGGTTG	CAAGCCTACGCTTGCAATGCGACG
	197	GAGCTGACGTCACCATCAGAGGAA	TTCCCTGTATGGTACGTCAGCTC
	198	GGAGGCTGGGGTCGCGCTTAAGT	ACTTAAGCGCAGCCCCAGCCTCC
	199	TTGTGGGAAACCGCACTAGCTGGCT	AGCCAGCTAGTGC
25	200	CCCTCGCACTGTGTTACCCCTTT	GGTTCACAGGCAACAGTGCAGGG
	201	TCATTGACTCGAACCGCACAACG	CGTTGTGCGGATTGAGTCAATGA
	202	ACAGGGGTTGGCCTCGTACGTAC	GTACGTACGAAGGCCAACCCCTGT
	203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGATGTTGCACGGCCT
	204	GGGCGTGGTCACGTAATTGGC	GCCAATATTACGTGACCAACGGCC
30	205	GCGCGGACATGAAACGACAAGGCC	GGCCTTGTGTTCATGTCGGCGC
	206	CTTATTGGGTGCCGGTGTGGATT	AATCCGACACCGGCACCAATAAG
	207	GGGGCGGTTACCAAAAAATCCGAT	ATCGGATTTTGTAAACCGCCCC
	4	CCGTCGCATACCGCTACGATCAA	TTGATCGTAGCCGGTATGCGACGG
	5	ATGGCCGTGCTGGGACAAGTCAA	TTGACTTGTCCCCAGCACGGCCAT
35	210	ACGAAAAAAAGTGTGCGGATCCCCT	AGGGGATCCGACACTTTTCGT
	211	CCAAGTACACCGCACGCTTAA	TAAACATGCGTGC
	212	ATCGTGCCTGGAGTGTGCACTA	GGTACTCCACGTGCTGCCAGCAGAT
	213	TCCAGATAACGCCCGAACCTTGA	TCAAAGTTGGGGCGGTATCTGGA
	214	TCTGCTGGCAGCACGTGAAGTGGC	GCCACTTCACGTGCTGCCAGCAGA
	215	TTGAAATTGCTCTGCCGTAGTCA	TGACTGACGGCAGAGCAATTCAA
40	216	AGTCAGGCAGAGATGTCAGGCAGC	GCTGCCTGAACATCTCGCCTGACT
	217	ACAAGCCGACGTTAAGCCGCCCA	TGGGCGGGCTTAACGTCGGTTGT

	218	CCCTAATGAGGCCAGTAACCTGCA	TGCAGGTTACTGGCCTCATTAGGG
	219	GTGAGACACACATCCCCTCCAATG	CATTGGAGGGGATGTGTGTCTCAC
5	220	CGACGGATGCAGAGTTAGTGGTC	GACCACTGAACTCTGCATCCGTCG
	221	CCCGCATGCCTGGCGGTATTACAA	TTGTAATACGCCAGGCATGCGGG
	222	TTAGCAAAGCGGCCGCGTTAGCAA	TTGCTAACGGCGCCGTTGCTAA
	223	CCCGACACGGGTCAAGCGTAATAAT	ATTATTACGCTGACCGTGTCGGG
	224	GCGACGGCCCTGAGGTATGTCGTC	GACGACATACCTCAGGGCCGTCGC
	225	CAAAAGTGTGTTCCCTTGCCTTG	CAAGCGCAAGGAAACACACTTTG
10	226	TCTCGAACGACAGCCCCGGTTATTG	CAATAACCGGGCTGTGCTTCGAGA
	227	ATGCTAACCGTTGGCCATGGAAC	AGTTCCATGGCCAACGGTTAGCAT
	228	CTTGCAGGAGTGTAGCCCAGCGGT	ACCGCTGGCTAACACTCCGCAAG
	229	TGCTCCCTAGGCGCTCGGAGGAGT	ACTCCTCCAGCGCCTAGGGAGCA
	230	CCAATGCCCTTGAGTAAGCGATGG	CCATCGCTTACTCAAAGGCATTGG
15	231	AGCAGATAACGTCCAATGACGCC	GGCGTCATTGGGACGTTATCTGCT
	232	TTGACCATTACGTGTTGCGCCCAT	ATGGGCGAACACGTAATGGTCAA
	233	TCGCGTATTCGCGGAATTGCTCTG	CAGACGAATTCCGAAAATACGCGA
	234	CTGCGTGTCAACAATGTCCCGCAG	CTGCGGGACATTGTTGACACGCAG
	235	TCTGGTGCCACGCAAGGTCCACAG	CTGTGGACCTTGCCTGGCACCAAGA
20	236	CTCCGGGAGGTCACTTAATTGCGG	CCGCAATTAAGTGACCTCCGGAG
	237	TTTCGTGATTGCCGGAGGAGGC	GCCTCCTCCGGCAATCACGAAAA
	238	TCGGGATGTAGCTGGGCTACCGG	CCGGTAGCCCCAGCTACATCCCGA
	239	CGAGCCAACGCAAACACGTCTTG	CAAGGACGTGTTGCCTGGCTCG
	240	GCAAAGCCTTGTGGGCGGTAGT	ACTACGCCAACAAAGGTTTGC
25	241	ATTCGACCGGAAATGAGGTCTCG	CGAAGACCTCATTCCGGTCGAAT
	242	TTCGCTTGCTGAGTTGCTCTGTT	GAACAGAGCAACTCAGCAAGCGAA
	243	CGCGTGAAGACCCCATTCCCGAGT	ACTCGGGAAATGGGTCTTCACCGCG
	244	AACCGTATTGCGGGTCACTGTGG	CCACAAGTGACCGCGAACACGGTT
	245	GGGGCCAACCGTTGAGGCGTAT	ATACGCCCTGAAACGGTTGGCCCC
30	246	TTCGGCTGGCAGTCAAACGGCTT	AAGCCGTTGGACTGCCAGCCGAA
	247	GGGTGTGGTTAGAATGCACGGTC	GAACCGTGCAATTCTAACACACCC
	248	GCGAGGACCGAAACTAGACAAACGG	CCGTTTGTCTAGTTCGGTCCTCGC
	249	ACGCACCGGTGACCGAAGTTGCTG	CAGCAACTCGGTACCGCGTGGT
	250	TAAAAGTCGCTTGAAGGGGGGA	TCCCCCTTCAAAGCGACCTTTA
35	251	TGCGATCGCTAACTGCTGGGACAA	TTGTCCCAGCAGTTAGCGATCGCA
	252	GGAGGTATAAGCGGAGCGGCTCA	TGAGGCCGCTCCGTTATACCTCC
	253	ATGCTGACATGTCGTGCACTCGT	ACGAGGTGCACGACATGTCAGCAT
	254	TGTGGTTAAAGCGTCCGTTAACG	CGTTGAACGGACGCTTAACCACA
	255	CGTTCACACCGCGTAAGCTGCGT	ACGCAGCTACGCCGGTGTGAACG
40	256	CCTATCCCGCGAGAACTCTGTG	CACAGAAGTTCTGCCGGGATAGG
	257	GTCTGCACTCACGCAGCGGAGGGA	TCCCTCCGCTGCGTGAGTCAGAC
	258	GCACGAGTTGGTGCTCGGCAGATT	AATCTGCCGAGCACCAACTCGTGC

	259	AACGTCGACGACACACGTCGTC	GACGAACGTGTGTCGTGCGACGTT
5	260	ATGCGCGCTTATCCTAGCATGGTC	GACCATGCTAGGATAAGCGCGCAT
	261	TCACGTTTCGTCTCGACATGAGG	CCTCATGTCGAGACGAAAACGTGA
	262	TGTGCCTCATCCTAGGATACGGC	GCCGTATCTAAGGATGAGGCACA
	263	AGGTGGTGTGGGTCAACCGCTTA	TAAAGCGGTTGACCCACACCACT
10	264	CTGGATCGAAGGGACTGCAAGCTC	GAGCTTGAGTCCTCGATCCAG
	265	TAGATCAACTCGCGTACGCATGGA	TCCATGCGTACGCGAGTTGATCTA
	266	GATCCTGCGGAGAAGAGAGTGCAG	CTGCACTCTCTCCGAGGATC
	267	TACGTGTGGAGATGCCCGAACCG	CGGTTGGGGCATCTCCACACGTA
15	268	GCGCTATGTCAATCGTGGCGTAG	CTACGCCACGATTGACATAGCGC
	269	AGCGAGGTTCTAGCGTCGACACC	GGTGTGACGCTAGAAACCTCGCT
	270	ACCCAGGTTTGCCGTTGGAAT	ATTCCACAAACGGCAAAACCTGGGT
	271	CCCTGTTAACGGCTCGTAGTC	GAGACTACGCAGCCGTTAACAGGG
	272	AGGCCGATTTCACCCGCCAATTG	GCAATTGGCGGGTAAATGGCCT
20	273	GAGCCCTCACTCCTGCCCTTGA	TCAAAGGGCAAGGAGTGAGGGCTC
	274	GGGTGGACATCCGCCTCGCAGTCA	TGACTGCGAGGCGGATGTCCACCC
	275	GATGGCTGAGAACCGTGCTACGAT	ATCGTAGCACGGTTCTCAGCCATC
	276	TCGACGTTAGGAGTGCTGCCAGAA	TTCTGGCAGCACTCCTAACGTGCA
	277	CGAATGGGTCTGGACCTTGATAG	CTATGCAAGGTCCAGACCCATTG
25	278	GTGCACCAGACATTGAACTCGGA	TCCGAGTTCGAATGTCGGTGAC
	279	AGAGGCCCCGTATATCCCATCCAT	ATGGATGGATATAACGGGGCTCT
	280	AACGCCTGTTAGAGCATCAGCGG	CCGCTGATGCTCTGACAGGCCTT
	281	AAGGCTAACACGCTATGTGCGC	GCGCACATAGCGTGTGAGCCTT
	282	AGTCCGTGTTGCCAGATTGGCTCG	CGAGCCAATCTGGCAACACGGACT
30	283	ATGTCCCATGTAAAGACGCGTGTG	CACACCGTCTTACATGGACAT
	284	ATGGAGTCTGCTCACGCCAAAGG	CCTTGGCGTGAGCAGACTCCAT
	285	CGGCCTCCAACAAGGAGCACTAAC	GTTAGTGCTCCTGTTGGAGGCCG
	286	CAGAGCCGTGGCAACATTGCGAGC	GCTCGCAATGTTGCCACGGCTCTG
	287	TCATTGAATGAGGTGCGCACCGG	CCGGTGCACCTCATTCAAATGA
35	288	GACGTACCGGAAGCGCCGTATAAA	TTTATACGGCGCTTCCGGTACGTC
	289	ATGCGAGCAATGGATCCGGATT	GAATCCGGATCCCATTGCTCGCAT
	290	AGAGTGAGGCCTCCCTGACCAGTG	CACTGGTCAGGGAGGCCTCACTCT
	291	CGCACCGTAAGTAGATTGCCCGC	GCGGGCAAAATCTACTTACGGTGCG
	292	TGAACCTTGAGCACGTCGTGCGC	GCGCACGACGTGCTCAAAGGTTCA
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	294	GAACGCCAACGGCACTAACACATC	GATGTGTTAGTGCCGTTGGCGTTC
	295	CCGACAGCAGCCAAGACGTCCCAG	CTGGGACGTCCTGGCTGCTGTCGG
	296	CATAAAAAACCTGGGCTCTGCG	CGCAGAGCCCCAGGTTTTATG
	297	TGCCAACTGTGCAGACCGGACTTA	TAAGTCCGGTCTGCACAGTTGGCA
	298	GGCGAAAGAGCGAAACCGGCTCGT	ACGAGCCGGTTCGCTCTCGCC
	299	GGGATGCGTATTTAGCGAACACG	CGTGGTCTGCTAAATACGCATCCC

	300	TGGGATTCAAGCGACCAAGTACGCAG	TCGCGTACTGGTCGCTGAATCCCA
	301	CCCGATATTCGCCCGGCCTATTCG	CGAATAGGCCGGCGAACATATCGGG
	302	CGAGAAAGATGCCTCACGCAACCAA	TTGGTTGCGTGAGGCATCTCTCG
	303	AACCTTGACCCGTGGATGACGCTA	TAGCGTCATCCACGGGTCAAGGTT
5	6	TTGCAACGGGCTGGTCAACGTCAA	TTGACGTTGACCAGCCC GTGCAA
	7	CGCATAGGTTGCCGATTCGTCAA	TTGACGAAATCGGCAACCTATGCG
	306	GCTTCCGGATGAACGGGATGGTTG	CAACCATCCC GTTCA TCCGGAAAGC
	307	CCCTCCATGTTCTCGAACGGTT	AAACCGTTGAGAACATGGAGGG
	308	TTGATGGGCGGCAATGCTCTGCT	AGCAAGAGCATTGCCGCCATCAA
	309	ATTGTGAGATGCGCAAATCCCC	GGGGAATTGGCGCATCTCACAAT
10	310	TCAGCACAGCCAGACGGTCAACTT	AAGTTGACCGTCTGGCTGTGCTGA
	311	ACTCCACTCCTCGGTGGCAAACTA	TAGTTGCCACCGAGGGAGTGGAGT
	312	TCTGGGCATGCCTGGACGGAGACG	CGTCTCCGTCCAGGCATGCCAGA
	313	TCTCAACTCCGGTACGACGAAACA	TGTTTCGTCTGACCGGAGTTGAGA
	314	TTGCGTGGTCAAAGCGAACGTG	CACGTTGCCCTTGACCA CGCAA
	315	AGACAGCGATCCGCGGGCTATGAT	ATCATGAGCCGCGGATCGCTGTCT
15	316	CGCGTCTCTAACTGAGAGCAGCCA	TGGCTGCTCTCAGTTAGAGACCG
	317	AGGCGCACATGTACGGACATTCA	CTGAATGTCGTACATGTGCGCCT
	318	GATGAGTGGCACGTCGGTGTAA	TTACACACCGACGTGCCACTCATC
	319	TGATCCATATTGTCGGACGTTGCG	CGCAACGTCGACAATATGGATCA
	320	ACCTGCCGGGAGTTCATAGGCTAG	CTAGCCTATGAACTCCGGCAGGT
	321	AGCATTGGCGTTTCCGCAACGA	TCGTTGCGAAAAACGCCAATGCT
20	322	GGTAATATTCA CGCGCGACCGCTCA	TGAGCGGTCGCGCTGAATATTACC
	323	ATAGCGTACGACGAGGTGACCGC	GCGCGTACCTCGTCGTACGCTAT
	324	TAGGTACCGATGCGTTGACGCTA	TAGCGTAAACCGCATCGTGACCTA
	325	ACTGCCGTACCTCTGGTTCTGGC	GCCAGAACAGAGGTACGGGAGT
	326	CCTTTGGCCTGAAGTTGCGTAGC	GCTACGACAACCTCAGGCCAAAGG
	327	GTGCCAACGAGCGTACGTGTTGTA	TACAACGATA CGCTCGTGGGCAC
25	328	AGGGCCTACGTGGCCTGGAGCAA	TTGCTCCAGGCCACGTAGGCC
	329	GGGTGCTACCATTCGATTAGTCG	CGGACTAATGCAATGGTAGCACCC
	330	ACCACGCGCGTACGTGTAACCGAG	CTCGGTTACACGTACGCGCGTGG
	331	CCATGATGCATTGGGTGCATTAG	CTAAATGCACCCAAATGCATCATGG
	332	GGTCGGCCCTACGAAACGTTCGA	TCGAACGTTCTCGTAGGGCCGGACC
	333	CCGTGTGGCTGGAGATTGCGTGT	TCACACGAATCTCCAGCCACACGG
30	334	GTTAGGGCGACGCATATTGGCACA	TGTGCCAATATGCGTCGCCCTAAC
	335	GGGTCA GTCAGGTGCGTTAGGATC	GATCCTAACGCACCTGACTGACCC
	336	GCCGTGAAGTCGAATGCGAGATCGA	TCGATCTGCAATTGACTTCACGGC
	337	GCCACCA CCCCAGTGCATTAGGTA	TACCTGAATGCACTGGGTGGTGGC
	338	GAGCTTAGTTGCGGTCA TCGGGC	GCCCGATGACCGCAA ACTAAGCTC
	339	TGTTTGCCGCCATTAGGGAGTAAC	GTTACTCCCTAATGGCGGCAAACA
35	340	GCTCCGCTGGATGTGCCGGTTAG	CTAAACCGGCACATCCAGCGGAGC

	341	CGGTAGCATGCGAGATCCCTGTTA	TAACAGGGATCTGCATGCTACCG
	342	CTACGCTCTACCAGTTGCCTGCGA	TCGCAGGCAACTGGTAGAGCGTAG
	343	GTGCCTCCTGCTTATTGCCAAG	CTTGGCAAATAACAGCAGGAGGCAC
5	344	TTGCGACTCGACTTGGACGAGTAG	CTACTCGTCCAAGTCGAGTCGCAA
	345	TCTGGGAGCTGTTACTCCAGCCA	TGGCTGGAGTAAACAGCTCCCAGA
	346	TGCACGCGGAACCTCCCTTACCAT	ATGGTAAAGGGAGTCCCGGTGCA
	347	TGGCAGCAAATGAATCGAAAGCAC	GTGCTTCGATTCAATTGCTGCCA
	348	AACTGGTACGCGGTACAGCGAAC	CTTCGCTGTACCGCGTCACCAGTT
	349	AGACGATTACGCTGGACGCCGTG	CGACGGCGTCCAGCGTAATCGTCT
10	350	ATGCCCTCCTCATGGAAAGGGTT	AACCCTTCCATGAAGGAGGGCAT
	351	ATTCTCGGAGCGTATGCGCCAGAA	TTCTGGCGCATA CGCTCCGAGAAT
	352	ATAGCGGAGTTGGGTACGCCAAC	GTTCGCGTACCCAAACTCCGCTAT
	353	ACCTACGCATACCGCTGGCGAGG	CCTCGCCAAGCGGTATCGTAGGT
	354	GATTACCTGAATGCCAAGCGAGC	GCTCGCTGGCCATTAGGTAATC
15	355	CCTGTTAGCATCACGGCGCTTAGG	CCTAAGCGCCGTATGCTAACAGG
	356	CGGAATGATGCGCTCGACAACGCT	AGCGTTGTCGAGCGCATTCCTCG
	357	TGAGAGAGGC GTTGGTTAAGGCAA	TTGCCTTAACCAACGCCCTCTCA
	358	AAGCAGGCCAAGGGATACTCCCG	CGAGGAGTATCCCTCGCCTGCTT
	359	TCACGACAGACGGGCCGAGATTAC	GTAATCTCGGCCGTCTCGTGA
20	360	AAGCAATTGGCCTCGTTTGTA	TCACAAAACGAGGCCAATTGCTT
	361	GCTGGTTGCGGTAGGATCGCATAT	ATATGCGATCCTACCGCAACCAGC
	362	TTGTGAATCCGTTCTGCCCCGAC	GTCGGGGACAGAACGGATTACAA
	363	TGGGCTCCTCTGAGGCAGATGGC	GCCATCTCGCCTCAGAGGAGGCCA
	364	GGATAGAGTGAATCGACCGCAAC	GTTGCCGGTCGATTCACTCTATCC
25	365	TGCACCGAACGTGCACGAGTAATT	AATTACTCGTGCACGTTGGTGCA
	366	GCCAGTATTCTCGGGTGTGGACG	CGTCCAACACCCGAGAACACTGGC
	367	TCGCTACCTAACGACGGGCCATAC	GTATGGCCCGGTCTAGGTAGCGA
	368	TGGCATTGACGAGCAGCAGTCAGT	ACTGACTGCTGCTCGTCAATGCCA
	369	CGCGTCCCAGCGCCCTGGAGTAT	ATACTCCAAGGGCGCTGGACGCC
30	370	ATGAAG CCTACCGGGCGACTCGT	ACGAAGTGC CCGGTAGGCTTCAT
	371	CCAGACAGATGGCCTGGAACCATG	CATGGTTCCAGGCCATCTGCTGG
	372	TGGCGTGGGACCATCTCAAAGCTA	TAGCTTGAGATGGTCCCACGCCA
	373	CCGCATGGAACACGTGTCAAGGT	ACCTTGACACGTGTTCCCACGCC
	374	GCCCAC TCGTCAGCTGGACGTAAT	ATTACGTCCAGCTGACGAGTGGC
35	375	ATTACGGTCGTGATCCAGAAAGCG	CGCTTCTGGATCACGACCGTAAT
	376	TGCAGGGT GAGCACCTACGAGAGA	TCTCTCGTAGGTGCTCACCTCGCA
	377	GGGCCGCATTCTGATGTCCATT	GAATGGACATCAAGAACATGCC
	378	CCTCGGATGTGGCTCTCGCTAG	CTAGGCAGAGGCCACATCCGAGG
	379	TAGGCATGTTGGCGTGAGCGCTAT	ATAGCGCTACGCCAACATGCC
40	380	CGATACGAACGAGGATGTCCGCCT	AGGCGGACATCCTCGTTGTATCG
	381	TACGCCGGTTAGCACGGTGCCTA	TAGCGCACCGTGCTAACCGCGTA

	382	CATACGATGTCCGGGCCGTGCGC	GCGACACGGCCGGACATCGTATG
	383	ATCCGCAGTTGTATGGCGCTTAT	ATAACGCGCCATACAACACTGCGGAT
	384	GGGTAAGGGACAAAGATGGGATGG	CCATCCCACATTTGTCCCTAACCC
5	385	ATTGGAGTGTTTGGTGAATCCGC	GCGGATTCAACCAAAACACTCCAAT
	386	GAACCGAGCCAACGTATGGACACG	CGTGTCCATACGTTGGCTCGGTT
	387	GCCGTCAAGCTTAAGGTTTGGC	GCCCCAAACCTTAAGCTTGACGGC
	388	ACCTGCTTTGGTGGGTGATATG	CATATCACCCACCCAAAAGCAGGT
	389	AATCGTGGGCGCAGCAAACGTATA	TATACGTTGCTGCCACGATT
10	390	GTCGCCGGATTGCTCAGTATAAGC	GCTTATACTGAGCAATCCGGGAC
	391	ACCCGTGATGCTTCCTCCTCAGA	TCTGAGGAGGAAGCATCGACGGT
	392	ATCCGGGTGGGCATACAAGAGAT	ATCTCTTGTATCGCCACCCGGAT
	393	TTCCGCATGAGTCAGCTTGAAAA	TTTCAAAGCTGACTCATGCGGAA
	394	GCAAAGTCCCCTGGCAAGCCGAT	ATCGGCTTGCAGTGGACTTGC
15	395	CGACCTCGGCTTCATCGTACACAT	ATGTGTACGATGAAGCCGAGGTG
	396	CTCATGAGCGCAGTTGCGTGAG	CTCACGCACAACCGCGCTCATGAG
	397	CAGATGAAGGATCCACGGCCGGAG	CTCCGGCCGTGGATCCTTCATCTG
	398	TCAAAGGCTTGGATACAGCCGT	ACGGCTGTATCCAAGAGCCTTGA
	399	TCCGCTAATTCCAATCAGGGCTC	GAGCCCTGATTGAAATTAGCGGA
20	8	CCGTTTGGGTGTCCTTGCTCAA	TTGAGCAAGGACGACCGCAAACGG
	9	TTCGCTTCGTGGCTGCACTCAA	TTGAAGTGCAGCCACGAAAGCGAA
	402	CTTAGTTGGGCGCGGTATCCAGA	TCTGGATACCGCGCCCCAACTAAG
	403	GCTCTAATGCCGTGGAGTCGAAC	GTTCCGACTCCACGGCATTAGAGC
	404	CCGATTACAATTGACTGACCGCA	TGCGGTAGTCATTGTAATCGG
25	405	AGACGTACGTGAGCCTCCGTGTC	GACACGGGAGGCTACGTACGTCT
	406	AATGGAGCGATACGATCCAACGCA	TGCGTTGGATCGTATCGCTCCATT
	407	GGAGGCCTGTACTGATAGCGTA	TACGCCATACAGTACAGCGCCTCC
	408	TGTTTTGAATTGACCACACGGGA	TCCCGTGTGGTCAATTAAAAACA
	409	CATGTCTGGATGCGCTCAATGAAG	CTTCATTGAGCGCATCCAGACATG
30	410	GCCCCCTAATCCGACACCCAGTT	AAACTGGGTGTCGGATTAGCGGGC
	411	CCATTGACAGGAGAGCCATGAGCC	GGCTCATGGCTCTCCTGTCAATGG
	412	GAATCACCGAATACCGACTCGTT	AACGAGTCGGTATTGGTGATTTC
	413	AACCAGCCGAGTAGCTTACGTG	CGACGTAAGCTACTGCGGCTGGTT
	414	TTTCTGAGGGACACGCCGGCGTT	AACGCCCGCGTGTCCCTCAGAAAA
35	415	GGTGTCCGTTGATCGATCCTCC	GGAGGGATCGATCAAACGGAGCACC
	416	CCGCTTAGGCCATCTGAGCCA	TGGCTCAGAGTATGGCTAACGGG
	417	TAAGACATACCGACGCCCTGGCCT	AGGCAAGGGCGTCGGTATGTCTTA
	418	GTTCCCGACGCCAGTCATTGAGAC	GTCTCAATGACTGGCGTCGGAAC
	419	TAAAAGTTCGCGGAGGTGGGCT	AGCCCGACCTCCCGCAAACTTTA
40	420	CGGTCCAGACGAGCTGAGTCGGC	GCCGAACTCAGCTCGTCTGGACCG
	421	CGGCGTAGCGGCTACGGACTAAA	TTAAGTCCGTAGCCGCTACGCCG
	422	GCTTGGATGCCCATGCGGCAAGGT	ACCTTGCCGATGGCATCCAAGC

	423	AGCGGGATCCCAGAGTTCGAAAA	TTTCGAAACTCTGGATCCCGCT
	424	GAGCTTGAGAGCGAGGTCATCCTC	GAGGATGACCTCGCTCTCAAGCTC
	425	GCATCGGCCGTGGACCATATTG	GAATATGGTCAAAACGGCCGATGC
5	426	CATAGCGCTGCACGTTGACCGC	GCGGTGAAACGTGCAGCGCTATG
	427	ACCCGACAACCACCAATTCAAAA	TTTTGAATTGGTGGTGTGGGT
	428	GCGAACACTCATAAGAGCGCCCTG	CAGGGCGCTTATGAGTGTTCGC
	429	CCGCCGAGTGTAGAGAGACTCCGA	TCGGAGTCTCTACACTCGGCGG
	430	GACATCGGGAGCCGGAAACATGAG	CTCATGTTCCGGCTCCGATGTC
10	431	TCGTGTAGACTCGGCACAGGC	ACGCCTGTCGCCGAGTCTACACGA
	432	ATGCGCATATACTGACTGCGCAGG	CCTGCGCAGTCAGTATATGCGCAT
	433	ACAAGCGAACCCGAGTTGATGA	TCATCAAAACTCGGGTTCGCTTGT
	434	GCATGAGACTCCGCGAAGACATGT	ACATGTCTCGCGGAGTCTCATGC
	435	TCCTACATGTCGCGTCACGATCAC	GTGATCGTACGCGACATGTAGGA
15	436	GACCGATCGCGAAGTCGTACACAT	ATGTGTACGACTTCGCGATGGTC
	437	GTCGCCAGGACTGGGCCGATGTGA	TCACATCGGCCAGTCCTGGCGAC
	438	ACCGATAAGACTTGCATCCGAACG	CGTTCGGATGCAAGTCTTATCGGT
	439	TCCATAACCAGTCCGAAGTGCCGG	CCGGCACTTCGGAUTGGTTATGGA
	440	ACGCGCCCTGCATCTCGTATTTAA	TTAAATACGAGATGCAGGGCGCGT
20	441	AGACCGCATCAATTGGCGTACCC	GGTACGCGCCAATTGATGCGGTCT
	442	AGAGGCTTGGCAAGTAGGGACCC	AGGGTCCCTACTTGCCAAGCCTCT
	443	GCAATGGACGCCAGACGATACCGG	CCGGTATCGTCTGGCGTCCATTGC
	444	GCTGGACTTAGTCGTGTTGCCGG	CCGCCGAACACGACTAAGTCCAGC
	445	AGGCATCGTCCGGATTGCTCCCT	AGGGAGCAATCCGGCACGATGCQT
25	446	TGCGCATGTCGACGTTGAACAAAG	CTTTGTTAACGTCGACATGCGCA
	447	TTCGGGTACATCCGATGCCATAC	GTATGGCATCGGATGTGACCCGAA
	448	ACCCATGCCCGAAAGCGATGTTG	CAACATCGTTCCGGCGATGGGT
	449	AAGCGCTGACTCGGTAAGAATCA	TGATTCTAGCCGAGTCAGCGCTT
	450	ACTTCCAAGTCCTGACCGTCCGA	TCGGACGGTCAAGGACTTGGAACT
30	451	TCTCAATATTCCCGTAGTCGCCA	TGGGCAGACTACGGAAATTGAGA
	452	AACAGTTCCCTTTTCCGGCGC	GGGCCAGGAAAAAGAGGAACGTGTT
	453	CGTCCTCCATGTTGTCACGAACAG	CTGTTCGTACAAACATGGAGGACG
	454	TGCCGAGACCTACCTGTCTTGCT	AGCAAAGACAGGTAGGTCTGCCA
	455	ATGGACGGCTTCGCACTCCCTT	AAGGAGGACTGCGAAGCCGTCCAT
35	456	TGAACGCTTCTATGGGCCACGTA	TACGTGGCCATAGAAAGCGTTCA
	457	TGAACCTGCCGCGAGCGATAACC	GGTTATCGTCGCGGGCAGGGTCA
	458	GTTCTTGCAGGATGAATCAGGACC	GGTCCTGATTGATCGCGCAAGAAC
	459	AGGGTACGTGTCGAGCTCGCGT	ACGCGAAGCTGCGACACGTACCC
	460	ACCCCTGCTCCGCCATGTCTCA	TGAGAGACATGGCGGAGCAAGGGT
40	461	GGGACAAGGATTGAAGCTGGCGTC	GACGCCAGCTCAATCCTGTCCC
	462	TGTCGTTGCTCCGAGTACCATTTG	CAATGGTACTCGGGAGCAACGACA
	463	GTTGTCCGAGACGTTGTGTCAGC	GCTGACACAAACGTCTCGGACAAC

	464	GCTGGTGAACACTCACGAACCGCT	AGCGGTTCTGTGAGTGTTCACCAGC
	465	GCAGACAGGGCAAATCGGTGCAAA	TTTGCACCGATTGCCCTGTCTGC
5	466	CCCATCACACGAGTGGCGACTTT	AAAGTCGCCACTCGTTGTGATGGG
	467	GCTTCTACAGCTGGCGTCTAGCG	CGCTAGCACGCCAGCTGTAGAACGC
	468	GAATGTGTGCCGACCATTCTAGCC	GGCTAGAATGGTCGGCACACATTC
	469	CCAGCGGAAGTTAGAGCTCTGTGG	CCACAGAGCTCTAACCTCCGCTGG
	470	TTTTACCGACCCTCCATGTCGG	CCGACATGGAGTGGTCGGTAAAAA
	471	GCGGCTATGTGATGACGGCCTAGC	GCTAGGCCGTCTACATAGCCGC
10	472	AGTACACGGGCGTGTAGCGCTCC	GGAGCGCTAACACGCCCGTGTACT
	473	TCCTGTGTGGTGGCGCACTCCCAC	GTGGGAGTGCGCCACCACACAGGA
	474	CCAACTAACCAATCGCGCGGATGA	TCATCCGCGCGATTGGTTAGTTGG
	475	AGTGAGTGACCAAGGCAGGAGCAA	TTGCTCCTGCCCTGGTCACTCACT
	476	CATCTTCGCGGAGTTATTGCGG	CCGCAATAAAACTCCCGAAAGATG
15	477	CTTCGTCCGGTTAGTGCACAGCA	TGCTGTCGCACTAACCGGACGAAG
	478	CTCACGAAAACGTGGGCCGAAAT	ATTCGGGCCCCACGTTTCGTGAG
	479	CGCAGCAGCTGAACCTCTAGCATTG	CAATGCTAGAGTTAGCTGCTGCG
	480	AGGAGACATACGCCAAATGGTGC	GCACCATTGGCGTATGTCCT
	481	ATTGAGAACTCGTGCAGGGAGTTG	CAAACCTCCGCACGAGTTCTCAAT
20	482	CTCTTGTAGGCCAGGAGGAGCA	TGCTCCTCCTGGCCTACAAAGAG
	483	GCCGCAGGGTCGATAATTGGTCTA	TAGACCAATTATCGACCCCTGCGC
	484	AAACGCCGCCCTGAGACTATTGGG	CCCAATAGTCTCAGGGCGCGTT
	485	CTGAGTTGCCTGGAACGTTGGACT	AGTCCAACGTTCCAGGCAACTCAG
	486	CGGATGGGTTGCAGAGTATGGGAT	ATCCCATACTCTGCAACCCATCCG
25	487	CTGACCTTGGGGTTAGTGCAGT	ACCGCACTAACCCCCAAAGGTAG
	488	GGAAATGAGAACCTTACCCAGCG	CGCTGGGTAAGGTTCTCATTCC
	489	AACGCATCGTCCGTCAACTCATCA	TGATGAGTTGACGGACGATGCGTT
	490	TGGAGAGAGACTTGGCCATTGTT	AACAATGGCGAAGTCTCTCTCCA
	491	TTGCGCTCATTGGATCTTGTCAAG	CCTGACAAGATCCAATGAGCGCAA
	492	AGCGCGTTAACGACGGCAACATT	AATGTTGCCGTGCTTAACGCGCT
30	493	AGCCAGTAAACTGTGGCGGTGT	ACAGCCGCCACAGTTACTGGCT
	494	CGACTGATGTGCAACCAGCAGCTG	CAGCTGCTGGTTGCACATCAGTCG
	495	GGTTGCTCATACGACGAGCGAGTG	CACTCGCTCGTCGTATGAGCAACC
	10	GTCCAACGCGCAACTCCGATTCAA	TTGAATCGGAGTTGCCGCGTTGGAC
	11	TTGCCGACCGTCCGTCTCAA	TTGAGATGACGGACGGTGCAGGCAA
35	498	AGAACCTCCGCGCCTCCGTAGTAG	CTACTACGGAGGCGCGGAGGTTCT
	499	AAAGGAGCTTCGCCAACGTACC	GGTACGTTGGCGAAAGCTCTT
	500	AGTGATTGTGCCACTCCACAGCTC	GAGCTGTGGAGTGGACAGCGTCTC
	501	GCGATCGTCGAGGGTTGAGCTGAA	TTCAAGCTCAACCCCTCGACGATCGC
	502	GGGAGACAGCCATTATGGCCTCG	CGAGGACCATATGGCTGTCTCCC
40	503	GAGACGCTGTCACTCCGGCAGAAC	GTTCTGCCGGAGTGACAGCGTCTC
	504	CCACCGGTCGCTTAAGATGCACTT	AAGTGCATCTTAAGCGACCGGTGG

	505	CGGCATAACGTCCAGTCCTGGAC	GTCCCAGGACTGGACGTTATGCCG
5	506	AAGCGGAACGGGTTAACCGAGGT	ACCTCGGTATAACCGTCCGCTT
	507	TGCACACTAGGTCCGTCGCTTGAT	ATCAAGCGACGGACCTAGTGTGCA
	508	AGGGAACCGCGTTCAAACTCAGTT	AACTGAGTTGAACCGGGTCCCT
	509	GAATTACAACCACCCGCTCGTGT	AACACGAGCGGGTGGTTGTAATT
	510	TTCAGTGTCTACGAAGCATGGATT	AATCCATGCTCGTGAGCACTGAA
	511	TTAGTTGGCGTTGGGACTTCACC	GGTGAAGTCCCACGCCAACTAA
10	512	AATGCGACCTCGACGAGCCTCATA	TATGAGGCTCGTCGAGGTCGCATT
	513	CCGAAACCGTTAACGTGGCGACA	TGTGCGCCACGTTAACGGTTCGG
	514	TAAAGTAACAAGGCGACCTCCCGC	GCGGGAGGTGCGCTTGTACTTTA
	515	TAATGATTTAGTCGCGGGGTGGG	CCCACCCCCGCGACTAAAATCATTA
	516	GGCTACTCTAACGTGCCGCTCAGG	CCTGAGCGGGCACTTAGAGTAGCC
	517	TGGCGGACGACTCAATATCTCACG	CGTGAGATATTGAGTCGTCGCCA
	518	GGGCGTTAGGCGTAATAGACCGTC	GACGGTCTATTACGCCAACGCC
15	519	GCCACCTTAGACGGCGGCTCTAG	CTAGAGCCGCCGCTAAAGGTGGC
	520	GAGATGTGTAAACGTGCAGGCACC	GGTGCCTGCACGTTACACATCTC
	521	TAGCTCGTGGCCCTCCAAGCGTGT	ACACGCTTGGAGGGCACGAGCTA
	522	GTGTCGGCGCTATTGGCCTTACCC	GGTAAGGCCAAATAGCGCCGACAC
	523	CCAGGGAAAGCAACTGGTTGCCATT	AATGGCAACCAGTTGCTCCCTGG
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	525	GCAAACCCGGTAACCCGAGAGTTC	GAACCTCGGGTTACCGGGTTTGC
	526	GCAAATGGCGTCATGCACGAAACGT	ACGTTCGTGCATGACGCCATTGC
	527	AGTACTTCGCGCCCCAGTTAGGG	CCCTAAACTGGCGCGAAAGTACT
	528	AAGATCTGCGAGGCATCCGGCTT	AAGCCGGATGCCTCGCAGATCTT
25	529	GCAAGTGTATCGCACAGTGCATT	ATACGCACTGTGCGATACTTGC
	530	CCGACAAGGCCTCAATTCTTG	CAGAATGAATTGAGGCCCTGTCGG
	531	GTCTCGTCTCAACTTAAGGCGCG	CGCGCCTTAAAGTTGAGACGAGAC
	532	ATCCAGAGATCCGTTTGCAGCGT	ACGCTGAAAACGGATCTCTGGAT
	533	GTCACCAAGGAGGGAAAGTTACCC	GGGTGAAACTCCCTCTGGTGAC
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	535	ATGCCGGACACGCATTACACAGGC	GCCTGTGTAATGCGTGTCCGGCAT
	536	TGGGCCGCTTGGCGCTTCTAGA	TCTATGAAAGGCCAAGCGGCCA
	537	CCTAGCGCGAGCTTTACTGACCAG	CTGGTCAGTAAAGCTCGCGCTAGG
	538	TTGGCCAGGAATATGGTCTCGAGA	TCTCGAGACCATATTCCGGCAA
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	540	AACTTGCTCATTCTCAAGCCGACG	CGTCGGCTTGAGAATGAGCAAGTT
	541	ACGTCAGCGATTGTGGCGAAATAT	ATATTCGCCACAATCGCTGACGT
	542	ACGGCCTCGTCAGCACATGCATC	GATGCATGTGCTGACGCAGGCCGT
	543	ATACCTCCGCAGAACCATCCGTT	AACGGAATGGTTCTGCGGAGGTAT
40	544	AGTTCGCGGTCCCACGATTCACTT	AAGTGAATCGTGGGACCGCGAAGT
	545	TGCTCAATTGTGCAGAAAACGCC	GGCGTTCTGCACAAATTGAGCA

	546	TTATCGCGAGAGACGCCGTGTCC	GGACACGGTCGTCTCGCGATAA
	547	GACCGCACGTGAGTAGTGGAAAGCG	CGCTTCAACTACTCACGTGCGTC
	548	ATGGTAGGGCATTGGGCTTCCT	AGGAAAGCCCAATGCCCTACCAT
5	549	CCAAATATAGCCGCGGGAGACAT	ATGTCTCCGCGGGCTATATTGG
	550	GCAAACCTGATTGAATCGTGCCC	GGGCACGATTCAATCAGGGTTGC
	551	TAGCGTCTTGCCTGAAACCATGGG	CCCATGGTTTACGCAAGACGCTA
	552	CCACCCCCACAGCGCTGGACTCTT	AAGAGTCCAGCGCTGTCGGGGTGG
	553	ACGAGCACTGAAGGCTGCTTACG	CGTAAAGCAGCCTCAGTGCTCGT
10	554	CATATCAGCGTCGCTAGCTCGCG	CCCGAGCTAGACGACCGCTGATATG
	555	TGATCCGGACCGGCTAGACTAAT	ATTAGTCTAGCCGGTCCGGGATCA
	556	GGCCCCGACACTACAGGGTAATCA	TGATTACCTGTAGTGTGGGGCC
	557	GGCTCCAGGGCGAGATTATGAATG	CATTCTATACTCGCCCTGGAGCC
	558	CAAATCCGATGGCGGAAAATTA	TAATTTCCGCCATCGGATTTG
15	559	CACAGGCCATAGGGAGCAAGCTA	TAGCTTGCTCCCTATGCGCCTGTG
	560	TAGCTATTGCCCGATGGCTACT	AGTAGCCCATCGGGCAATAGCTA
	561	TGGTACCGGGTCCATAGCAAGTCG	CGACTTGCTATGGACCGCGTACCA
	562	GACGCTGTGGCTGGAAACTGTTC	GAACAGTTCCGAGCCACAGCGTC
	563	CCTGGGTTCGCCGCGTGGTAAGTG	CAGTTACCACGCCGGAACCCAGG
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	565	TTCGCGGATTGCTGCCGCATAACA	TGTTATGCGGCAGCAATCCCGCAA
	566	AAAAATGGCACCGAAGTTGAGGCA	TGCCTCAACTCGGTGCCATTTT
	567	CATTCCGCGCGAGTTGAAATCCAG	CTGGATTCAACTCGCGCGGAATG
	568	ACGCACGTTTTGGCACGGTTAA	TTAACCGTGCCAAAAACGTGCGT
25	569	TGTCCATGACGTCGTTCTCTGGT	ACCAGAGAAACGACGTACGGACA
	570	TCTCAGTCGGACTCGTATGCCAGA	TCTGGCATAACGAGTCCGACTGAGA
	571	CTCCAAACGCACACATCAAGCATC	GATGCTTGATGTGCGTTGGAG
	572	TTCAACCAAGCGGGGTGTCGTGA	TCACGAACACCCCGCTGGTTGAA
	573	GGTGTGCGAGGGTGGTGACCTCGA	TCGAGGTCAACCACCCCTCGACACC
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	575	CCGAGGACTTACGTCGTCCCAGGA	TCCTGGCAGACGTAAGTCCTCGG
	576	GCCCAATCCAGTTCTATGCGCCC	GGGCGCATAAGAACTGGATTGGC
	577	CGGGTTAACCCACGCAAGTTATGA	TCATAACTCGTGGTTAACCG
	578	TGATTAGCGCTCAATACACGCGTG	CACCGTGTATTGAGCGCTAATCA
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	580	GCGCCACAAGATTACATGTCACT	AATGACATGTGAATCTTGTGGCGC
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	582	CGCGGTGTTGTCTAGGTGCCGG	CCGGCACCTAGACAAAACACCGCG
	583	CAACATTGGTGGCACTCCATCC	GGATGGAGTGCACCAATGTTG
40	584	CGATACGCGCCGGTTGTTAACATC	GATTTAACAAACGGCGCGTATCG
	585	GGCTATAAACGTGCGGACTGCTCC	GGAGCAGTCCGCACGTTATAGCC
	586	TGGGTAAATCACTATTGCGCGGTT	AACCGCGCAATAGTGATTACCCA

587	GTCTTCATCGGCCCGCGCAAGCTA	TAGCTTGCCTGGGCCGATGAAGAC
588	GCGACACACCCCTGTACTCTGATGC	GCATCAGAGTACAGGGTGTGTCGC
589	GTAGCAGGGTCCGCAAGACCAAGC	GCTTGGTCTTGCCTGGACCCTGCTAC
590	TCGCCAACGCGAGGTAACTGCCAT	ATGGCAGTTACCCCTGCCTGGCGA
591	ACTCCGAAGCTTCGAGCGGCACGA	TCGTGCCGCTCGAAGCTTCGGAGT
12	CATCGTCCCTTCGATGGGATCAA	TTGATCCCCTCGAAAGGGACGATG
13	GCACGGGAGCTGACGACGTGCAA	TTGACACGTCGTCAGCTCCGTGC
594	ATCATCCCACGGCAGAGTGAAGAG	CTCTTCACTCTGCCGTGGGATGAT
595	CGCTGGACTGGCCTATCCGAGTCG	CGACTCGGATAGGCCAGTCCAGCG
596	CGGTCTCAGCAACACTGTCGCAA	TTTGCACAGTGTGCTGAGACCG
597	CGAACGTTCTCCGATGTAATGGCC	GGCCATTACATCGGAGAACGTTCG
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599	AGCTCATTCGGAGACGGAACACC	GGTGTCCGCTCTCGGAATGAGCT
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601	ACTCGAACGGACGTTAACCTCCA	TGGGAATTGAAACGTCCGTTGAGT
602	CTGCATGGTGTGGGTGAGACTCCC	GGGAGTCTCACCCACACCATGCAG
603	CCCGCAGTGTGGATGGCGTGTGA	TCAACACGCCATCCACACTCGCGG
604	AATGTGTCGGCTTAAGCCGGGTG	CACCCGGCTTAGGACCGACACATT
605	TAAGACGAGCCTGCACAGCTGCG	CGCAAGCTGTCAGGCTCGTCTTA
606	GGCGTGGGAGGATAAGACGATGTC	GACATCGTCTTATCCTCCCACGCC
607	TGCTCCATGTTAGGAACGCACAC	GTGGTGCCTTAACTGGAGCA
608	CGGTGTTGGTCGGACTGACGACTG	CAGTCGTAGTCCGACCAACACCG
609	CCCGCGCTATCTATCAGATCTGGG	CCCAGATCTGATAGATACGCGCGG
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611	ACTTGACATCGCTGGTAGATCCGG	CCGGATCTACCCAGCGATGCAAGT
612	TGCTTACGCAGTGGATTGGTCAGA	TCTGACCAATCCACTGCGTAAGCA
613	ATGCAGATGAACAAATGCCGAAT	ATTGGCGATTGTTCATCTGCAT
614	GCAATTCTGGGCCATGTATTGTC	GACGAATACATGGCCAGAACATTGC
615	AGGGTTCTTACCGCTCGACATGG	CCATGTCGACCGCTAAGGAACCCCT
616	GTGGAGCTAATCGCGAGCCTCAGA	TCTGAGGCTCGCGATTAGCTCCAC
617	TCGTTAGTCTACCGGCAATGATCC	GGATCATTGCCGGTGAGACTACGA
618	TTATAGCAGTGCCTGCGCAATGCTCG	CGAACAGTGGCGACTGCTATAA
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621	CATTAGCCCCTGTCGGTAACGT	ACAGTTACCGACAGCGGGCTAATG
622	GGAAAGAAACTCAGACCGCAATG	CATTGCGCTCTGAGTTCTTCC
623	CGACTCGCTGGACAGGAGAACGT	ACGATTCTCCTGTCCAGCGAGTCG
624	CATGATCCTCTGTTACCCCGCGG	CCGCGGGTGAAACAGAGGATCATG
625	GGCGTAGCGCTCTAAAGCTTCGG	CCGAAGCTTTAGAGCGCTACGCC
626	AGTGTGATGCCATCAGGCCGTATAC	GTATACGGGCCTGATGGCATCACT
627	TATGGAAAGGGCAACAGCGCTATC	GATAGCGCTGTTGCCCTTCCATA

	628	CTGTGGTTGATGGAGGAATCCACAC	GTGTGGATCCTCCATCAACCACAG
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	630	CAGGCCCGAACCACCGCGTTACAG	CTGTAACCGCGTGGTCGGCCTG
	631	GGCGCAATGGGCGCATAAATACTA	TAGTATTATGCGCCCATTGCGCC
	632	GGTCAATTGCGCTACATGCCCTA	TAGGGCATGTAGCGCGAATTGACC
	633	GATGGTGGACTGGAGCCCTCCGC	GCGGAAGGGCTCCAGTCCACCATC
	634	CCGCGCATAGCGCAATAGGGGAGA	TCTCCCTATTGCGCTATGCGCGG
	635	TCTTCTGGCTGTCCGGCACCCGAA	TTCGGGTGCCGGACAGCCAGAAGA
10	636	CGCGTTCGCAATTACGGGCCCTTA	TAAGGGCCCGTGAATTGCGAACGC
	637	TCGTTTCGGCCTTGGAGAGTATCG	CGATACTCTCAAGGCCGAAACGA
	638	AGGTGCAAGTGCAAGGCGAGAGGC	GCCTCTCGCCTTGCACTTGCACCT
	639	CGCCAGTTCGATGGCTGACGTTT	AAACGTCAGCCATCGAAACTGGCG
	640	GCTTACCGCCGATCCAGATATC	GATATCTGGGATCGGCGGTAAAGC
	641	GTGCTTGACGAAGAGGCGAAATGT	ACATTCG CCTT CGTCAAGCAC
15	642	CAGTCCGTGCGCTTCATGCTCTA	TGAGGACATGAAGCGCACGGACTG
	643	TACCGCGTAAGAGCCTACCCCTCGCG	CGCGAGGGTAGGCTTACCGCGTA
	644	GGCGAGTCTTGTGGGACATGTGT	ACACATGTCCCCACAAGACTCGCC
	645	CCAAGCGAACGAGCGTGTCTAT	ATAGACACGCTCGCTCGCTTGG
	646	GCCGTAGTTGCTTCAACCGAAC	GTTCGGTGAAGAGCAACCTACGGC
20	647	AAATCCCGCGATGTGCCGTGAGGCT	AGCCTCACGGCACATCGGGATTT
	648	GGCTCGCACCCGTACCAATTAG	CTAAATTGGTACGGGTGCGAACGC
	649	TGTAGAGTCCCACGTAGCCGGCAT	ATGCCGGCTACGTGGACTCTACA
	650	CACTAGTCTGGGCAAGGTGCTATT	AATGCACCTTGGCCAGACTAGTG
	651	TGTACTCGGCAGGCCAATAGATT	AATCTATTGCGCCTGCCAGTACA
25	652	AACGGGTATCGGAAGCGTAAAGC	GCTTTACGCTTCCGATACCGTT
	653	CGGACTGCCGTTTGCAGTTGAG	CTCAACTGCAAACGGGCAGTCCG
	654	ATCGTTCAGCACTGGAGCCCGTAA	TTACGGGCTCCAGTGCTGAACGAT
	655	ATGCATCGAACTAGTCGTGACGGC	GCCGTCACGACTAGTTCGATGCAT
	656	TTCCAGGCATTAAGGAGAGGGAGC	GCTCCCTCTCTTAATGCCCTGGAA
30	657	GTGCGACATCTACTCCACGATCCC	GGGATCGTGGAGTAGATGTCGAC
	658	CTCATCGTCTAACACGAGAGCCC	GGGCTCTCGTGTAGGACGATGAG
	659	AATGGCACTTCGGCCGTGATGCAA	TTGCATACCGCCGAAGTGCCATT
	660	CCGTGGGAGGGAAATCCAACCGAGG	CCTCGGTTGGATTCCCTCCCACGG
	661	AAATTCTCGTTGGTACGGCTCAT	ATGAGCCGTCACCAACGAGAATT
35	662	TTGCTCTTATCCTTGCCTGGCG	CGCCCAGGACAAGGATAAGAGCAA
	663	TTAAGGATCAGGCGGAGCTGCAG	CTGCAAGCTCCGCCTGATCCTAA
	664	CGCGACTAAGGTGCTGCAACTCGA	TCGAGTTGAGCAGCACCTAGTCGCG
	665	GCTCGATTTCACGGCCCGTTGTC	GAACAACGGGCCGTGAAATCGAGC
	666	AGCAGAGTGCCTGCAGAGGCTAA	TTAGCCTCTGCAACGCACTCTGCT
40	667	TGGAGGTGAGGACGACGTGCACTA	TAGTGCACGTCGTCCTCACCTCCA
	668	AACCGTTAGGGTACATTGCGCGT	ACCGCGAATGTACCCCTAACCGGT

	669	TATGATCGCTCGGCTCACAGTTG	CAAACGTGAGCCGAGCGATCATA
	670	GACTTTTGCAGAAACGTATGGT	ACCATGACGTTCCGCAAAAGTC
5	671	TGTCGGTTATTCCACCTGCAAGGA	TCCTTGCAGGTGGAATAACCGACA
	672	CTATGGTTGCACTGCGCCGTCGA	TCGACGGCGCAGTGCAAACCATAG
	673	AGCAGGGAAATTCAATCGTCGCA	TGCGAACGATTGAATTCCCTGCT
	674	CCTAACCGAGCGCTTAGCATTCC	GGAAATGCTAAGCGCTCGGTTAGG
	675	CCCGACCCTAACTCGCATTGAATA	TATTCAATGCGAGTTAGGTCGGG
	676	TTGCTTAATGGTGACGCCACGGAT	ATCCGTGGCGTCACCATAAGCAA
10	677	GATGCTGCCGTGTTAGTCACG	CGTGAACAAACACGGCGAGCATC
	678	TCGGATGACGAGTTCCATGACGG	CCGTATGAAACTCGTCATCCGA
	679	ATGCGGTCTACTTCTGATCGGG	CCCGATCGAGAAAGTAGACCGCAT
	680	TTGCGAGGCTAACGACACGGTAAA	TTTACCGTGTGCTTAGCCTCGCAA
	681	AACTTAATTACCGCCTCTGGCGCC	GGCGCCAGAGGCGGTAAATTAGTT
15	682	GTGACCGCGAACCTGTTCCGACAG	CTGTCGGAACAAGTCGCGGTAC
	683	TGCGGATTACCGATTGCTCTAA	TTAAGAGCGAACCGTAATCCGCA
	684	TGATAGGGGCCACGTTGATCAGA	TCTGATCAACGTGGCCCCATCA
	685	TCGCTCCGTAGCGATTATCGTAG	CTACGATGAATCGCTACGGAGCGA
	686	TGTCAGCTGGTAGCCTCCGTTGA	TCAAACGGAGGCTACAGCTGACA
20	687	AGCGTCGCATGACGCTTACGGCAC	GTGCCGTAAGCGTCATGCGACGCT
	14	AGACGCACCGCAACAGGCTGTCAA	TTGACAGCCTGTTGCGGTGCGTCT
	15	CGTGTAGGGTCCCCTGCTGTCAA	TTGACAGCACGGGACCCCTACACG
	690	GTCGCATTCTGCACTGGCTTCGCC	GGCGAACGCCAGTGCAGAATCGAC
	691	TGATTAGGTGCGGTCCCGTAGTCC	GGACTACGGGACCGCACCTAATCA
25	692	AAGGGACCTGGGTGACGGCGAGA	TCTCGCCGTACCCAAGGTCCCTT
	693	TCAAATGGCCACCGCGTGTCAATT	GAATGACACCGCGTGGCATTGTA
	694	CTCCGACCGACCAATAATAGCCGC	GGGGCTATTATTGGTCGTGGAG
	695	GGCTATTCCCGTAGAGAGCGTCCA	TGGACGCTCTACGGGAATAGCC
	696	TGGATAACCTCTCGGTCCATCCAC	GTGGATGGACCGAGAGGTTATCCA
30	697	GACCGCTGTACGGGAGTGTGCCCT	AAGGCACACTCCCGTACAGCGGTC
	698	GCCACAGAGTTTAGCAGGGACCC	GGGTCCTGCTAAACTCTGTGGC
	699	CCCACGCTTCCGACCACTGACCT	AGGTCACTGGTCGGAAAGCGTGGG
	700	CATTGACACAATGCGGGGACTGAT	ATCAGTCCCCGCATTGTGTCATG
	701	AGCCACTCGACAGGGTCCAAAGC	GCTTGGAAACCTGTCAGTGGCT
35	702	CAGGATGAGCAAAGCGACTCTCCA	TGGAGAGTCGCTTGCTCATCCTG
	703	CAAGGTATGGCTGGGCCCTAACG	GCTTACGGCCCCAGACCATACCTG
	704	GGTGTTCGGCCCTAAACTCTTCGG	CCGAAAGAGTTAGGCCAACACC
	705	TTTAGTCGGACCCCTGTGGCAATT	GAATTGCCACAGGGTCCGACTAAA
	706	CACACGTTCCGACCGCCTGAAC	GTTCAAGGCTGGTCGGAAACGTGTG
40	707	CTGGACGAACCTGGCTCCTCGTAC	GTACGAGGAAGCCAGTCGTCAG
	708	TTCACAATCCGCCGAAACTGACC	GGTCAGTTTCGGCGGATTGTGAA
	709	AACAGGATATCCGCGATCACGACA	TGTCGTGATCGCGGATACCTGTT

	710	TACGTGGATCCATTGCGCCGAGT	ACTCGGCCAATGGATCCGACGTA
	711	CATGGATCTCTCGGTTGATCGCC	GGCGATCAAACCGAGAGATCCATG
	712	AGCCAGGCGCGTATACGCTCGG	CCGAGCGTATACGCGCCTGGCT
5	713	ATTGGCACGTGTCGTGCCATGTT	AACATGGCACGACACGTGCCAAAT
	714	CCGCGTTGCACCACCTTGAGGTGC	GCACCTCAAAGTGGTCAACGCGG
	715	TTGGACGTGACAAGCATGGCGCTC	GAGCGCCATGCTTGTACGTCCA
	716	CTGAATCGCGCAAGTAAATGGGGG	CCCCCATTACTTGCACGATTCA
	717	GATAAGGTCCACCAGATTGCGCGC	GCGCGCAATCTGGTGGACCTTATC
10	718	CTAACAAATTGCCAACCGGGACGGC	GCCGTCCCCGGTTGGCAATTGTTAG
	719	GGTAACCTGGGTGCTTGCAGGTTA	TAACCTGCAAGCACCCAGGTTACC
	720	ATCGGAGCCACCATTGCGATTGGG	CCCAATGCGAATGGTGGCTCCGAT
	721	GTGAACCTGGCTTGCCTCAGGATTA	TAATCCTGGGGCAAGCCAGTTCAC
	722	AGGCGATAGCATGGTCCCATATGA	TCATATGGGACCATGCTATCGCCT
15	723	AACGGTATCGTGGCTAACGACGA	TCGTGCATTAGCCACGATACCGTT
	724	AGTAGTGGCCTCCAGATCGGCAA	TTGCCGATCTGGAGGACCAACTACT
	725	CCGTTGAATTGGACGGGAGGTTAG	CTAACCTCCCCTCCAAATTCAACGG
	726	GCATAAGTGGCGCATCGCGAAGGG	CCCTTCGCGATGCCGACTTATGC
	727	CGACAAGATGCAGCTGCTACATGC	GCATGTAGCAGCTGCATCTGTCG
20	728	TCGCAGTGATTCCCACCGATAAG	CTTATCGGTGGGAATCACTGCGA
	729	CAAGGCGAGTCCACTCGAGGGGAC	GTCCCCCTCGAGTGGACTCGCCTTG
	730	GCAACTTGCACGGCATAAGTGGCC	GGCCACTTATGCCGTGCAAGTTGC
	731	TCCGAGCTTGACGTTGCGACGTC	GACGTCGCGAACGTCAAGCTCGGA
	732	AGCGCTGGGCTGTGCTGCCATCTC	GAGATGGCAGCACAGCCCAGCGCT
25	733	TTCATGTGCGCTGAGTAACCTCGC	GCGAGGGTTACTCAGCGACATGAA
	734	CGAACCGCTAATGCCATTGTCAG	CTGACAATGGGCATTAGCGGTTCG
	735	CACGGAAAGGTGGGACAATCGCCG	CGGCGATTGTCCCACCTTCCGTG
	736	CACAGATGGAGACAAACGCGCCTT	AAGGCGCGTTGTCTCCATCTGTG
	737	TTTCGCAACTCGCTCCATAACCC	GGGTTATGGAGCGAGTTGCGAAAA
	738	ACGTTACGTTCCGGCGCTCTAA	TTAGAGGCCCGGAAACGTAACGT
30	739	TATCGGATTGCGTGGGTTCAATC	GATTGAAACCCACGCAATCCGATA
	740	CTTCCACAATTGCTGCGACGAC	GTGCGTCGACGACAATTGTGGAAG
	741	TGCACAAAGGTATGGCTGTCCGGC	GCCGGACAGCCATACCTTGTGCA
	742	TCCGATGCCAGTCCCCTTAAGA	TCTTAAGATGGGACTGGCATCGGA
	743	CTGAAACCGTGCATCGAGGTGA	TCACCTCGATTGACGGTTCA
35	744	CGGTGTTCCGCGTGTGCAAAAAT	ATTTTTGACACGCGGAACACCG
	745	TCTAGCAGGCCCTTGAATGCCA	TGGCGATTCAAAGGCCCTGCTAGA
	746	GAGTCACCTCTGAGACGGACGCCA	TGGCGTCCGTCTCAGAGGTGACTC
	747	TCTTCTGTCACTCTGCGAGCAGCAT	ATGCTGTCAGGATGACAGAAGA
	748	GGGGATGAAACCTGAAAGGGCCT	AGGCCCCTTCAGGTTCATCCGC
40	749	GGGGCCCCAAACTGGTATCAAGCC	GGCTTGATACCAAGTTGGGGCCCC
	750	GCATTGGCTTCGGATTCTCCTACA	TGTAGGAGAATCCGAAGCCAATGC

	751	AGGC GGCCCAACTGTGAGGTCTTG	CAAGACCTCACAGTTGGCCGCCT
5	752	ACACCATGTGCTCCCGCTGCAGT	ACTGCAGCGCGGAGCACATGGTGT
	753	ACGATGAACATGAATCGGGAGTCG	CGACTCCCATTGATGTTCATCGT
	754	CTGCATCCCTGTAGCAGCGCTCCG	CGGAGCGCTGCTACAGGGATGCAG
	755	GTGCCGTATTCGACCTGTGCGTT	AACGCACAGGTCGAAATACGGCAC
	756	GCAGTGCCTACTTCAGTTCAAAG	CTTTGAAGTGAAGTGCCTACTGC
	757	GCGATTTAAGCGATGCCCTGACG	CGTCAAGGCATCGCTAAATCGC
10	758	TAGGTGACCTAGGCTTGCTTGC GG	CCGCAAGCAAGCCTAGGTACCTA
	759	CTGGATAACCTTGCCCTGCGGGCGC	GCGCCGCACAGGCAAGGTATCCAG
	760	CCCCTTACGGCTCGTCGTCTATGC	GCATAGACGACGAGCCGTAAGGGG
	761	GCGCTTGCCTGCCGATGCGATGCATTA	TAATGCATCGCATCGGCAAGCGC
	762	TTTCTGTAAGCGGCTGGGTTCA	TGAACCCCAGGCCGCTTACAGAAA
	763	GGCTGAGGTGAGCGGTAAAGGATGA	TCATCCTTACCGCTCACCTCAGCC
15	764	TCTTGGCCTCCCCGATCTAATTG	CAAATTAGATCGGGGAGGCCAAGA
	765	GGAGGTAAACGCCGTGTACGTAGGA	TCCTACGTACACGGCGTTACCTCC
	766	GTAATCCATTGTGGCTGCGTCAA	TTGACGCAGCCACAAATGGATTAC
	767	CAAACCCATTCCAGCAGACGCCCTG	CAGGCCTGCTGCTGGAATGGTTG
	768	TAGGAGGAATTGGCATGCGGCG	CGCCCGCATGCCAAATTCCCTCTTA
20	769	ATAGGTAGGATGTGCCCGGCGTTG	CAACGCCGGCACATCCTACCTAT
	770	GCAAGTGCTTAGCTCGTCAGCCTC	GAGGCTGACGAGCTAACGACTTGC
	771	CTGGCTGTGCGCATCTCGTTAAC	GTAAACGAGATGCGACACAGCCAG
	772	CTAACGTCGTCTCGCGCAATCACT	AGTGATTGCGCGAGACGACGTTAG
	773	TTTCATAAACGTTGCCCGAGC	GCTCGGGACAACGTTATGAAAA
25	774	AGCAGGAGGACGAACCTCCGCTCC	GGAGCGGAGGTTCGCTCCCTGCT
	775	TTCAAGCACCATCGTGAATCAA	TTGGATTGCACGATGGTGTGTTGAA
	776	AGCGTCGCCAGTGATCGTAGTGG	CCACTAGCGATCACTGGCGACGCT
	777	TACATTCCCTGCCTCCGTGGCTT	AAGCCCACGGAGGCAGGGAAATGTA
	778	CGCTTCGCGTATTCACTAGCGGT	AACCGCTACTGAATACGCGAAGCG
	779	TCGGACCGTGCACACTCATTATA	TATAATGAGTGTGACCGCGTCCGA
30	780	TCTGAGCAGGCCAGCGCTCCAGCT	AGCTGGAGCGCTGGCTGCTCAGA
	781	TTGAATTGCCAAGCCCTGAAAGCC	GGCTTTCAAGGGCTTGGCAATTCAA
	782	AGTTTCGCCCTGATCGTCGGTG	CACCGACGCATCAAGGGAAAAGT
	783	GTTCATAGGCCACCGCGTGTAAA	TTAGCACCGCGTGGCCTATGAAAC
	16	CATCGCTGCAAGTACCGCACTCAA	TTGAGTGCAGGTACTTGCAGCGATG

TABLE 4

Seq. ID No.	Decoder Sequence (5'-3') + 5' T	Probe Sequence (5'-3') + 5' T
17	TTTCGCCGTCGTGTAGGCCTTCAA	TTTGAAAAGCCTACACGACGGCGAA
18	TGTTCCCAGTGAAGCTGCGATCTGG	TCCAGATCGCAGCTTCACTGGGAAC
19	TTACTGGCATGGAATCCCTACGC	TGCGTAAGGGATTCCATGCCAAGTA
20	TACTAGCATATTCAAGGGCACCGGC	TGCCGGTGCCTGAAATATGCTAGT
21	TGAACGGTCAATGAACCGCTGTGA	TTCACAGCGGGTTCAATTGACCGTTC
22	TGCGGCCTGGTCAATATGAATCG	TCGATTCATATTGAACCAAGGCCGC
23	TGATCGTTAGAGGGACCTTGCCCCGA	TTCGGGCAAGGTCCCTTAACGATC
24	TTGGACCTAGTCCGGCAGTGACGAA	TTTCGTCACTGCCGGACTAGGTCCA
25	TATAAACTACCCAGGACGGCGGAA	TTTCCGCCCCTGCCTGGTAGTTAT
26	TCATCGGTTCGCGCCAATCCAGATA	TTATCTGGATTGGCGCGAACCGATG
27	TGTCGGGCATAGAGCCGACCACCT	TAGGGTGGTGGCTCTATGCCGAC
28	TCTTGGGTCATGATTACCGTGCTA	TTAGCACGGTGAATCATGACCCAAG
29	TTGCCCTAACGTGCTAATCAGCAGCG	TCGCTGCTGATTAGCACGTTAGGCA
30	TCGCATGTTGGAGCATATGCCCTGA	TTCAAGGGCATATGCTCCAACATGCG
31	TAGCCACTGCATCAGTGTGTTCAA	TTTGAACACGCACTGATGCAGTGGCT
32	TGGTTGTTTGAGGCGTCCCACACT	TAGTGTGGGACGCCCTAAAACAACC
33	TTCGACCAAGAGCAAGGGCGGACCA	TTGGTCCGCCCTTGCTCTGGTCA
34	TGACATCGCTATTGCGCATGGATCA	TTGATCCATGCGCAATAGCGATGTC
35	TGAAATACGAAGTCTGCGGGAGTCG	TCGACTCCCGCAGACTCGTATTC
36	TTGTCATGAATGATTGATCGCGCA	TTCGCGCGATCAATCATTGACAGCA
37	TATATCGGGATTGCTTCCGGTGAA	TTTCACCGGGAACGAATCCCGATAT
38	TGCGAGCGTACCGAAGGGCTAGAA	TTTCTAGGCCCTCGGTACGCTCGC
39	TTTACCGGCAGCGGACTTCCGAATT	TAATTCGGAAGTCCGCTGCCGGTAA
40	TGTAATCGAGAGCTGCGCGCGTCT	TAGACGGCGCGCAGCTCTGATTAC
41	TCCTGTTAGCGTAGGCGAGTCGATC	TGATCGACTGCCCTACGCTAACAGG
42	TTAGCGGACCGGCAGAAATGAGTCC	TGGAACTCATTCTGCCGGTCCGCTA
43	TGGTACATGCACTACGCGCACTCGG	TCCGAGTGCACGTAGTCATGTACC
44	TAATTGATCTGGACTCCCGCGGT	TTACCGGGAGTCCGAGATGAATT
45	TGCCAAATCTGGATTGGCAGGAATG	TCATTCTGCCAATCCAGATTGGC
46	TTGCATTTCGGTTGAGGCACATCC	TGGATGTGCCTCAACCGAAAATGCA
47	TCCGCTCAATTACCATGCTTCGCT	TAGCGAAGGCATGGTGAATTGAGCGG
48	TCTCGGAAAGGTGCAACTTGGTGT	TACACCAAAGTTGCACCTTCCGAG
49	TAATTGACCAAGCAGAACGTCCCAT	TATGGGACGTTCTGCTGGTCAATT
50	TGCCAGAGTCTAACCTCACGGGAT	TATCCCGTGAGGTTGAGACTCTGGC
51	TCCAACAACTGGAACGGAACCCGC	TGCGGGTCCCGTCCAGTTGGTGG
52	TGAGAACTGATCGCTGAGGGCATG	TCATGCCCTCAGCGATCAGTTCTC
53	TGGCACACTAGACTTGTGGCACCGA	TTCGGTGCCACAAGTCTAGTGTGCC

	54	TTCACATCCAAATATGGTCCGCGAA	TTTCGCGGACCATAAATGGATGTGA
	55	TGTCTGCCGGTGTGACCGCTTCATT	TAATGAAGCGGGTCACACCGGCAGAC
5	56	TCATCGCAGAGCATAAACACCCCTCA	TTGAGGGTGTTATGCTCTGCGATG
	57	TGTTGGTATCTATGGCAGAGGCGGA	TTCCGCCTCTGCCATAGATACCAAC
	58	TACGAGGTGCCGCTGAGGTTCCATT	TAATGGAACCTCAGCGGCACCTCGT
	59	TGGAATGAGTGGACCCAGGCACATT	TAATGTGCCTGGGTCCACTCATTC
10	60	TTGTCATATGCGTCCGTGCGTCT	TAGACGACACGGACGCATATTGACA
	61	TTGATGAGCCTCAGGGTACGAGGCA	TTGCCTCGTACCCCTGAGGCTCATCA
	62	TCACCGCGGTGTTCCCTACAGAATGA	TTCATCTGTAGGAACACCGCGGTG
	63	TTTGTGCCAATGGTGTCCGCTCGG	TCCGAGCGGACACCATTGGCAACAA
	64	TTTAACCTGCGTCTGCCCTTCTT	TAGGAAAGGGGCAGACGCAGGTAA
15	65	TAGGCGCGTCTGCCTAGTGAAC	TCGTCACTAAGGCAGGAACGCCCT
	66	TTAGGGCGATGGCACGAAGCTCAA	TTTGAAGCTCGTGCCTACGCCCTA
	67	TTGCATAGAGCCAAAGTCGGCGATG	TCATGCCGACTTGGCTATGCA
	68	TTTGGAGAGGCAAGGTGGCCACACGA	TTCCGTGTGCCACCTGCCTCTAA
	69	TTCCGCATTGTGAGAAAAAACGAGC	TGCTCGTTTTCTCACAATGCGGA
	70	TGGCGGTTCCGTAGCTATAGGTGC	TGCACCTATAGCTACGGAAACGCC
20	71	TGGTAAAATTTCGTAGCCACGGC	TGCCCCTGGCTACGAAATTTCACC
	72	TCCGACGGAGGATGAAGACAATCAC	TGTGATTGCTTCATCCTCCGTCGG
	73	TCCAGTTGGCCCAATTGCCAAA	TTTTGGCGAATTGGGCCAAACTGG
	74	TGGATCTATTAGGCCGTGCGCACAG	TCTGTGCGCACGGCTAATAGATCC
	75	TCGGATGTCACCGTTGGACTTCA	TTGAAAGTCAAACGGTGACATCCG
25	76	TATCGCAAATCCTGCTCGTCCCTAA	TTTAGGGACGAGCAGGATTGCGAT
	77	TCAGGGCATGCAATAATCGAGGTT	TGAACCTCGATTATTGCATGCCCTG
	78	TCATGCGTTGATATATGGGCCAAG	TCTTGGGCCATATATCACCGCATG
	79	TCAGCTGCAGCTTGTGACCAACAC	TGTGGTTGGTCACAAGCTGCAGCTG
	80	TTTGTATGTCTGCCGACCGCGACC	TGGTCGCCGGTCGGCAGACATAACAA
	81	TGATGGCGCCCGTTGATAGGTATGG	TCCATACCTATCAACGGCGCCATC
30	82	TATGAGAATGCCGGCAATCTGCTA	TTAGCAGATTGCCGGGATTCTCAT
	83	TATTTGCACTGACCGCAGGCTCGT	TCACGAGCCTCGGGTCAGTGAAAT
	84	TCAGGGAGAACGGTTAACGTTCCCGT	TACGGGAACCTAACCGTTCTCCCTG
	85	TAGGCCGGGATCGAGGAGTTGGT	TACCAAACCTCTCGATGCCGGCCT
	86	TACACGGTGGTCTCTGATAGCGACC	TGGTCGCTATCAGAGACCAACGTGT
	87	TGTGCAACGCCGAGGACTTCATCA	TTGATGGAAGTCCTGGCGTTGCAC
35	88	TTCGGTGCCGTAGCCATTCCGAT	TATCGGAATGGCTATCAGGCACCGA
	89	TTGAAATACCAACACAGCCAATTGGC	TGCCAATTGGCTGTGTGGTATTCA
	90	TGCATCGTGTACATGACTGCCGCGA	TTCGCGGCAGTCATGTACACGATGC
	91	TCAGTGTCTAACGGCGCGTGAA	TTTCACGCCGCCGTTAGAACACTG
	92	TCGCTTGCAACGTTGACCTACTCT	TAGAGTAGGTGCAACGTTGCAAGCG
40	93	TCGAAAAACTAGTGGCTGCCGCG	TCGCAGGCCACTAGTTTCG
	94	TCTTCAGGGAACTGCCGGAGTCG	TCGACTCCGGCAGTCCCTGAAAG

	95	TTTGTGGCCTTCTGTAAAGGCACG	TCGTGCCTTACAAGAAGGCCACAA
5	96	TTCCACGAACGGCGACCCGTTGCT	TAGACAAACGGGTCGCCGTTGGA
	97	TCGACCTTGACGAAACCTAACGAG	TCTCGTTAGGTTCTGTCAAGGTCG
	98	TGTGCAGCTTCACGAGGCCAGCCTGA	TTCAGGCTGGCTCGTAAGCTGCAC
	99	TCGCTTCGTGCGAATAGACGATGA	TTCATCGTCTATTGACGAAAGCG
10	100	TTGCGCTTACAGGCTCTAGTGGTC	TGACCACTAGGAGCCTGTAAGCGCA
	101	TCACCGCCTAGTCGGATCGCATA	TTATGCGATCGCAGTAAGCGCGTG
	102	TCGGAGGGAGGGAGCTAGCCTTCGA	TTCGAAGGCTAGCTCCCTCCCTCCG
	103	TGCATCCGGCCTGTTGATGACGCC	TAGGCCTCATCAACAGGCCGGATGC
10	104	TAGGCCAATCGATCTATTGCCGAG	TCTCGGCAATAAGATCGATTGGCCT
	105	TCCTTCCAATGATTGACATACGCCA	TTGGCGTATGCAATCATTGGAAGG
	106	TAACACTTGATCAGGCCGGTCGTCT	TAGACGACCCGCCGATCAAGTGTT
	107	TTGGAATCAAGGCCGTAAGGACAG	TCTGTCCTTACGGCCTTGATTCCA
15	108	TGCTCCCGTAACCTGTCCACCAGTG	TCACTGGTGGACAGGTTACGGGAGC
	109	TAGGGTGAATGGCCGCTACCGCTGA	TTCAGGGTAGCGGCCATTCACT
	110	TTGTTGAAGCGAGCTAAAACGGCCA	TTGGCCGTTTAGCTCGCTTCACAA
	111	TCAGCGCTCCAGAATTGACAGCAAT	TATTGCTGTCAATTCTGGAGCGCTG
20	2	TTTCGAAGGCCACGTCCCTTCAA	TTTGAAGGGACGTGCGCTTCGAA
	3	TAACCGTGGGAATGGGACATCAA	TTTGATGTCCCATTCCCCACCGCGTT
	114	TCACGAGATACCGGCGTAAGGGTGG	TCCACCCCTACGCCGGTATCTCGTG
	115	TCTACGGCAAACGTGTTGAATGGGT	TACCCATTCCACACGTTGCCGTAG
	116	TGTAGGGCGATGACGGCGAACTAC	TGTAGTTGCCCGTCATGCCCTAC
25	117	TAATCGACCTCCGCACACATTGCA	TTGCGAATGTGTGCGGAGGTCGATT
	118	TGAGTCAGCATGGCGGGAGATTG	TGAATCTCCGCCGCATGCTGACTC
	119	TAGATAAAGACGCTGGCACACAGGG	TCCC GTGTTGCCAGCGTCTTATCT
	120	TGGTACCTCAACCGCAACCACCTGT	TACAAGTGGTTCGCGTTGAGGTACC
	121	TAAGCGATGGCTACCCAAGAGCGAT	TATCGCTCTGGGTAGCCATCGCTT
30	122	TAGAGCTTATGCAGAACCAAGGGGCC	TGGCGCCTGGTTCTGCATAAGCTCT
	123	TATCGGTCTCACGCAGGGTTGGATA	TTATCCAACCCCTGCGTGAGACCGAT
	124	TTAGGTTGCCGCCAGAAGAACAT	TATGTTCTCTGGCGGGCAACCTA
	125	TCGGTGCTGTTGCAAAGCCTGTAG	TCTACAGGCTTGTCAACAGCACCG
	126	TTGATGAAAGTTGCGGCAGGACAC	TGTGTCCTGCCGCAAACCTTCATCA
35	127	TGTTGAGTGCAGGATGCAGCGATAG	TCTATCGCTGCATCCTGCACTCAAC
	128	TAACATTGCGCGGTCCACCAGGGTT	TAACCCCTGGTGGACCGCGCAATGTT
	129	TGGGCAAGTTAGAGAGGGCCAGAAGT	TACTTCTGGCCCTCTCTAACTGCC
	130	TTCGAGCTGGTCCCCGTAACTGT	TACACGTTCACGGGGACCGACTCGA
	131	TGTCTGGGGCCGCTTAGTAAAA	TTTTCACTAAGCGGCCCAAGAC
40	132	TACTGTTGGCCTGCTCTCATGTCCA	TTGGACATGAGAGCAAGCCAACAGT
	133	TAGGACCATTGGAAGGCGAAGATA	TTATCTCGCCTCCGAATGGTCT
	134	TCTGGGAGGCATCCGCTATAAGGA	TTCCCTTATAGCGGATGCCCTCCAAAG
	135	TAATAAACGGAACGCACCGCTACAG	TCTGTAGCGGTGCGTTCCGTTATT

	136	TTTGTACGTGCGGTCCCCATAAGCA	TTGCTTATGGGACCCACGTACAA
5	137	TCGCACCAAACGTAGTTCCCAGAC	TGTCTGGGAAACTCAGTTGGTGC
	138	TACCTGATCGTCCCCATTGGGAA	TTTCCAATAGGGAACGATCAGGT
	139	TGGAACAGAGGCGAGGGGACTGAGC	TGCTCAGTCCCCTCGCCTCTGTTCC
	140	TCCCTGCCCTGGCGTCTGGCTTAT	TATAAGCCGACACGCCAAGGCAGGG
	141	TACTCTGACACGCCAACCTCCGGAAG	TCTTCCGGAGTTGGCGTGTCAAGAGT
	142	TCTGACGGTTTCATTGGCGTGCC	TGGCACGCCGAATGAAAACCGTCAG
	143	TTGCGGTGGTTATTGGAGCTGGCC	TGGCCAGCTCCAATGAACCACCGCA
10	144	TGCATGGCCAACTAGTGACTCGCAA	TTTGCAGTCACTAGTTGCCATGC
	145	TAGGCCGTAAAGCGAATCTCACCTG	TCAGGTGAGATTGCTTACGGCCT
	146	TCGAATATTATGCCGAGAACCGCG	TCGCGGATTCTCGGCATAATATTG
	147	TACAGACGAGCTCCAACCATGA	TTCATGTGGTGGGAGCTCGTCTGT
	148	TGGACGGTTGTGCTGGATTGTCTG	TCAGACAATCCAGCACAACCGTCC
	149	TAAGGCTATTGAGTTGGTGGCG	TCGCCCAACCAACTCAATAGCCTT
15	150	TGATGGCCTATTGGAGATCGGGCC	TGGCCCGATCTCCGAATAGGCCATC
	151	TGATCCAGTAGGCAGCTTCATCCCA	TTGGGATGAAGCTGCCACTGGATC
	152	TAATAACTCGCGCGGGATGCTTCT	TAGAAGCATACCGCGCAGTTATT
	153	TGGAGGAGGTTGTCTGGAAAGCA	TTGCTTCCGAGACAAACCTCCCTCC
20	154	TCTTGGTATGGCACATGCTGCCG	TCGGGCAGCATGTGCCATACCAAAG
	155	TAGAAAGGCTCGAGCAACGGGAAC	TAGTTCCCGTTGCTCGAGCCTTCT
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	157	TCGTGGCGGCCACAGTTTGAGG	TCCTCCAAAAACTGTGGCCGCCACG
	158	TTGCAAGTTCAATCCATACGACGT	TACGTGCGTATGGATTGAACTGCAA
25	159	TGGCCCAAGCCCCAGACCATTAA	TTAAAATGGTCTGGGGCTTGGGCC
	160	TCGCCTGTCTTGCTCCGGACAAT	TATTGTCCGGAGACAAAGACAGGCG
	161	TTGAGGCAACAGGGGCCAAAAACTA	TTAGTTTGGCCCTGTGCTCA
	162	TAGCGGAAGTAGTCCTCGCTCGTC	TGACGAGCCGAGGACTACTCCGCT
	163	TGGCCCCAAGGCTTAGAGATAGTGG	TCCACTATCTCTAACGCTTGGGCC
30	164	TGCACGTGAAGTTAACCGCGATTC	TGAATCGCGGTTAACCTCACGTGC
	165	TAGCGGCAGAACGTTCCGTACGG	TCCGTCAAGGAACGTTCTGCCGCT
	166	TTCGTCGAGCAGACGAGATTGACG	TCGTGCAATCTCGTCTGCTGACGA
	167	TTCTTGCCCGTAACTGACTGCTT	TAAGCAGTCAGTTACCGGGCAAAGA
	168	TTTATGTGCCAAGGGTTAACCGA	TTCGGTTAACCCCTGGCACATAAA
	169	TTGTTACTGTGGTTCACGGCAGTCC	TGGACTGCCGTGAACCAACAGTAACA
35	170	TCGCGCCTCGCTAGACCTTTATTG	TCAATAAAGGTCTAGCGAGGCGCG
	171	TACAAATGCGTAGAGAGCTCCCAACT	TAGTTGGGAGCTCTCACGCATTGT
	172	TCGCGCAGATTAGACCGAATGT	TACATTGGGTCTATAATCTGCGCG
	173	TCAAATAACGCCGCTGAATCGGCGT	TACGCCGATTAGCGGGCGTTATTG
40	174	TCCTTCGTGCATCGGTATGATGTT	TAACATCATACCGATGCACGAAGG
	175	TTGAACACGAGCAACACTCCAACGC	TGCGTGGAGTGTGCTCGTGTCA
	176	TCAGCAGATCCTCGTAGCGGCGT	TACGACCGCTACGAAGGATCTGCTG

	177	TGGAACCTGGTAGTTGCGCTCAT	TATGAGGCACAACTCACCAGGTTCC
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	179	TCCCAACGTCACTGAAGCTCACAGT	TACTGTGAGCTTCAGTGACGTTGGG
	180	TTGTCAGAGCCCGCGACTCAGACGG	TCCGTCTGAGTCGCGGGCTCTGACA
	181	TTACACGAAGCCTCTCCGTGGTCCA	TTGGACCACGGAGAGGCTTCGTGTA
	182	TCTCAGAAGTCCTCGCGAAGTGGG	TCCCAGTTGCCCGAGGACTCTGAG
	183	TATCCTTTATCTACTCCGCGCGA	TTCGCCGGAGTAGATAAAAGGAT
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	185	TACTCTGAGGGAGTCTCTGGCACA	TTGTGCCAGAGACTCCCTGAGAGT
	186	TTGCCAGGTCCATCGAGACCTGTT	TAACAGGTCTCGATGGACCTGGCAA
	187	TTCCACTATAACTGCGGGTCCGTGT	TACACGGACCCCGCAGTTATAGTGG
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	190	TTAAAATAAGCGCCTGGCGGGAGGA	TTCCCTCCGCCAGGCCTTATTTA
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	192	TAGTTGCCAGGTACTGGCAAGTGC	TGCACTTGCCAGTACCTGGCAAAC
	193	TACAACGAGGGATGTCCAGCGGCAT	TATGCCGCTGGACATCCCTCGTTGT
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	195	TTAACCGATTTTGCAGCTTGCC	TGGCAGAGTCGCAAAATGGGTTA
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	197	TGAGCTGACGTCAACATCAAGGAA	TTTCCTCTGATGGTACGT
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	199	TTTGTGGGAACCGCACTAGCTGGCT	TAGCCAGCTAGTGC
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	203	TAGGCCGTGCAACATCACACAGGAT	TATCCTGTGTGATGTTGCACGGCCT
	204	TGGGCCGTGGTACGTAATATTGGC	TGCCAATATTACGTGACCACGGCCC
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	215	TTTGAATTGCTCTGCCGTAGTCA	TTGACTGACGGCAGAGCAATTCAA
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	218	TCCCTAATGAGGCCAGAACCTGCA	TTGCAGGTTACTGGCCTCATAGGG
	219	TGTGAGACACACATCCCCTCCAATG	TCATTGGAGGGGATGTGTCTCAC
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	221	TCCCGCATGCCTGGCGGTATTACAA	TTTGTAAACCGCCAGGCATGCCGG
	222	TTTAGCAAAGCGGCCGCCGTAGCAA	TTTGCTAACGGCGCCGCTTGCTAA
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	224	TGCGACGGCCCTGAGGTATGTCGTC	TGACGACATACCTCAGGGCGTCGC
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	229	TTGCTCCCTAGGCGCTCGGAGGAGT	TACTCCTCCGAGCGCCCTAGGGAGCA
	230	TCCAATGCCTTGAGTAAGCGATGG	TCCATCGCTTAACCAAAGGCATTGG
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25	241	TATTCGACCGGAAATGAGGTCTCG	TCGAAGACCTCATTCGGTCGAAT
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	248	TGCGAGGACCGAACTAGACAAACGG	TCCGTTGCTAGTTGGCTCTCGC
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	257	TGTCTGCACTCACGCAGCGGAGGGA	TTCCCTCCGGTGCCTGAGTGCAGAC
	258	TGCACGAGTTGGTGCTCGGAGATT	TAATCTGCCAGCACCAACTCGTGC

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	337	TGCCACCA CCCAGTGCATTCA GGTA	TTACCTGAATGCAC TGGTGGTGGC
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	434	TGCATGAGACTCCGCGAAGACATGT	TACATGTCTCGCGGAGTCTCATGC
	435	TTCCATACATGTCGCGTCACGATCAC	TGTGATCGTGACGCGACATGTAGGA
	436	TGACCGATCGCGAAGTCGTACACAT	TATGTGTACGACTTCGCGATGGTC
20	437	TGTCGCCAGGACTGGCCGATGTGA	TTCACATCGGCCAGTCCTGGCGAC
	438	TACCGATAAGACTTGCATCCGAACG	TCGTTGGATGCAAGTCTTATCGGT
	439	TTCCATAACCAGTCCGAAGTGCCGG	TCCGGCACTTCGGACTGGTATGGA
	440	TACCGGCCCTGCATTCGTATTTAA	TTAAATACCGAGATGCAGGGCGCT
25	441	TAGACCGCATCAATTGGCGCGTACC	TGGTACGCGCCAATTGATGCGGTCT
	442	TAGAGGTTGGCAAGTAGGGACCT	TAGGGTCCCTACTTGCCAAGCCTCT
	443	TGCAATGGACGCCAGACGATACCGG	TCCGGTATCGTCTGGCGTCCATTGC
	444	TGCTGGACTTAGTCGTGTTGGCGG	TCCGCCAACACGACTAAGTCCAGC
	445	TAGGCATCGTGCCGGATTGCTCCCT	TAGGGAGCAATCCGGCACGATGCCT
30	446	TTGCGCATGTCGACGTTGAACAAAG	TCTTGTCAACGTCGACATGCGCA
	447	TTTCGGGTACATCCGATGCCATAC	TGTATGGCATGGATGTGACCCGAA
	448	TACCCATGCCGGAAAGCGATTTG	TCAACATCGCTTCCGGCGATGGGT
	449	TAAGCGCTGACTCGGCTAAGAATCA	TTGATTCTAGCCGAGTCAGCGCTT
	450	TACTTCCAAGTCCTTGACCGTCCGA	TTCGGACGGTCAAGGACTTGGAAAGT
	451	TTCTCAATATCCCCTAGTCGCCA	TTGGGCGACTACGGGAATTGAGA
35	452	TAACAGTCCCTCTTTCTGGCGC	TGCGCCAGGAAAAAGAGGAACGTGTT
	453	TCGTCCTCCATGTTGACGAACAG	TCTGTTCGTACAAACATGGAGGACG
	454	TTGCGCAGACCTACCTGCTTGT	TAGCAAAGACAGGTAGGTCTGCGCA
	455	TATGGACGGCTCGCAGTCCTCCCT	TAAGGAGGACTGCGAAGCCGTCCAT
	456	TTGAACGCTTCTATGGCCACGTA	TTACGTGGCCATAGAAAGCGTTCA
40	457	TTGAACCCCTGCCGCGAGCGATAACC	TGGTTATCGCTCGCGGCAGGGTTCA
	458	TGTTCTTGCACGATGAATCAGGACC	TGGTCTGATTGACATCGCGCAAGAAC
	459	TAGGGTACGTGTCGAGCTCGCGT	TACCGCAAGCTGCGACACGTACCT
	460	TACCCCTGCTCCGCCATGTCCTCA	TTGAGAGACATGGCGGAGCAAGGGT
	461	TGGGACAAGGATTGAAGCTGGCGTC	TGACGCCAGCTCAATCCTTGTCCC
	462	TTGTCGTTGCTCCGAGTACCATTTG	TCAATGGTACTCGGGAGCAACGACA
	463	TGTTGTCCGAGACGTTGTGTCAGC	TGCTGACACAAACGTCTCGGACAAC

	464	TGCTGGTGAACACTCACGAACCGCT	TAGCGGTTCTGTGAGTGTTACCCAGC
	465	TGCAGACAGGGCAAATCGGTGAAA	TTTGCACCGATTGCCCTGTCTGC
5	466	TCCCACATACAACGAGTGGCGACTTT	TAAAGTCGCCACTCGTTGTGATGGG
	467	TGCTTCTACAGCTGGCGTGCTAGCG	TCGCTAGCACGCCAGCTGTAGAACG
	468	TGAATGTGTGCCGACCATTCTAGCC	TGGCTAGAATGGTCGGCACACATTG
	469	TCCAGCGGAAGTTAGAGCTGTGG	TCCACAGAGCTCTAACCTCCGCTGG
	470	TTTTTACCGACCCTCCATGTGG	TCCGACATGGAGTGGTCGGAAAAAA
	471	TGCGGCTATGTGATGACGGCTAGC	TGCTAGGCCGTACATCACATAGCCGC
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	474	TCCAACTAACCAATCGCGCGGATGA	TTCATCCGCGCGATTGGTTAGTTGG
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	476	TCATCTTCGCGGAGTTATTGCGG	TCCGCAATAAAACTCCGCGAAAGATG
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	478	TCTCACGAAAACGTGGGCCGAAAT	TATTCGGGCCCACGTTTCGTGAG
	479	TCGCAGCAGCTGAACTCTAGCATTG	TCAATGCTAGAGTTCAGCTGCTGCG
	480	TAGGAGACATACGCCAAATGGTGC	TGCACCATTGGCGTATGTCTCCT
	481	TATTGAGAACTCGTGCGGGAGTTG	TCAAACCTCCGCACGAGTTCTCAAT
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	483	TGCCGCAGGGTCGATAATTGGTCA	TTAGACCAATTATCGACCCCTGCGGC
	484	TAACGCCGCCCTGAGACTATTGGG	TCCCAATAGTCTCAGGGCGGCGTT
	485	TCTGAGTTGCCTGGAACGTTGGACT	TAGTCCAACGTTCCAGGCAACTCAG
	486	TCGGATGGGTGCAAGAGTATGGGAT	TATCCCATACTCTGCAACCCATCCG
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	489	TAACGCATCGTCCGTCAACTCATCA	TTGATGAGTTGACGGACGATGCGTT
	490	TTGGAGAGAGACTCGGCCATTGTT	TAACAATGGCGAAGTCTCTCTCCA
	491	TTTGCCTCATGGATCTTCAGG	TCCTGACAAGATCCAATGAGCGCAA
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	493	TAGCCAGTAAACTGTGGCGGCTGT	TACAGCCGCCACAGTTACTGGCT
	494	TCGACTGATGTGCAACCAGCAGCTG	TCAGCTGCTGGTTGCACATCAGTCG
	495	TGGTTGCTCATACGACGAGCGAGTG	TCACTCGCTCGTCGTATGAGCAACC
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	499	TAAAGGAGCTTCGCCAACGTACC	TGGTACGTTGGCGAAAGCTCCTTT
	500	TAGTGATTGTGCCACTCCACAGCTC	TGAGCTGTGGAGTGGCACAATCACT
	501	TGCGATCGTCGAGGGTTGAGCTGA	TTTCAGCTCAACCCCTGACGATCGC
	502	TGGGAGACAGCCATTATGGTCCTCG	TCGAGGACCATAATGGCTGTCTCCC
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	504	TCCACCGGTCGCTTAAGATGCACTT	TAAGTGCATCTTAAGCGACCGGTGG

	505	TCGGCATAACGTCCAGTCCTGGGAC	TGTCCCAGGACTGGACGTTATGCCG
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	507	TTGCACACTAGGTCCGTCGCTTGAT	TATCAAGCAGCGACCTAGTGTGCA
	508	TAGGGAACCGCGTTAAACTCAGTT	TAACTGAGTTAACCGGGTCCCT
	509	TGAATTACAACCACCCGCTCGTGT	TAACACGAGCGGGTGGTTGAATT
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	511	TTTAGTTGGCGTTGGGACTTCACC	TGGTGAAGTCCAACGCCAACTAA
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	514	TTAAAGTAACAAGGCACCTCCGC	TGCGGGAGGTCGCCTTACTTTA
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	516	TGGCTACTCTAACGTGCCGCTCAGG	TCCTGAGCGGGCACTTAGAGTAGCC
	517	TTGGCGGACGACTCAATATCTCACG	TCGTGAGATATTGAGTCGTCCGCCA
	518	TGGCGTTAGGC GTAATAGACCGTC	TGACGGTCTATTACGCCTAACGCC
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	520	TGAGATGTGAAACGTGCAGGCACC	TGGTGCCTGCACGTTACACATCTC
	521	TTAGCTCGTGGCCCTCCAAGCGTGT	TACACGCTTGGAGGGCACGAGCTA
	522	TGTGTCGGCGCTATTGGCCTTACC	TGGTAAGGCCAAATAGCGCCGACAC
	523	TCCAGGGAAAGCAACTGGTGCCTT	TAATGGCAACCAGTTGCTTCCCTGG
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	525	TGCAAACCCGGTAACCCGAGAGTT	TGAACCTCGGGTTACCGGGTTGC
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	527	TAGTACTTCGCGCCAGTTAGGG	TCCCTAAACTGGCGCGAAAGTACT
	528	TAAGATCTCGAGGCATCCGGCTT	TAAGCCGGGATGCCTCGCAGATCTT
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	535	TATGCCGGACACGCATTACACAGGC	TGCCTGTGTAATGCGTGTCCGGCAT
	536	TTGGGCCCTGGCGCTTCAAGA	TTCTATGAAAGGCCAAGGGCCA
	537	TCCTAGCGCAGCTTACTGACCAG	TCTGGTCAGTAAAGCTCGCGCTAGG
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	540	TAACTTGCTCATTCTCAAGCCGACG	TCGTCGGCTTGAGAATGAGCAAGTT
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	543	TATACCTCCGCAGAACCATCCGTT	TAACGGAATGGTTCTGGAGGTAT
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	545	TTGCTCAATTGTGAGAAAACGCC	TGGCGTTCTGCACAAATTGAGCA

	546	TTTATCGCGAGAGACGACCGTGTCC	TGGACACGGTCGTCTCTCGCGATAA
	547	TGACCGCACGTGAGTAGTGGAAAGCG	TCGCTTCCACTACTCACGTCGCGTC
	548	TATGGTAGGGGCATTGGGCTTCCT	TAGGAAAGCCCAATGCCCTACCAT
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	552	TCCACCCCCGACAGCGCTGGACTCTT	TAAGAGTCCAGCGCTGTCGGGGTGG
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	554	TCATATCAGCGTCGTCTAGCTCGG	TCGCGAGCTAGACGACGCTGATATG
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	556	TGGCCCCGACACTACAGGGTAATCA	TTGATTACCCCTGTAGTGTGGGGCC
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	562	TGACGCTGTGGCTCGAAACTGTTTC	TGAACAGTTCCGAGGCCACAGCGTC
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	573	TGGTGTGGAGGGTGGTGAACCTCGA	TTCGAGGTACCAACCCCTCCGACACC
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	575	TCCGAGGACTTACGTCTGCCAGGA	TTCCCTGGGACAGCTAAGTCCTCGG
	576	TGCCCAATCCAGTTCTATGCGCCC	TGGGCGCATAAGAACTGGATTGGC
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5	710	TTACGTCGGATCCATTGCGCCGAGT	TACTCGGCGCAATGGATCCGACGTA
	711	TCATGGATCTCTCGGTTGATGCC	TGGCGATCAAACCGAGAGATCCATG
	712	TAGCCAGGCGCGTATATACGCTCGG	TCCGAGCGTATATACGCGCCTGGCT
	713	TATTGGCACGTGTCGTGCCATGTT	TAACATGGCACGACACGTGCCAAAT
	714	TCCCGCGTTGCACCACTTGAGGTGC	TGCACCTCAAAGTGGTGCAACGCGG
10	715	TTTGGACGTGACAAGCATGGCGCTC	TGAGCGCCATGCTTGTACGTCCAA
	716	TCTGAATCGCGCAAGTAAATGGGGG	TCCCCCATTTACTTGCACGATTCAAG
	717	TGATAAGGTCCACCAGATTGCGCGC	TGCGCGCAATCTGGTGGACCTTATC
	718	TCTAACAAATTGCCAACCGGGACGGC	TGCCGTCCCCGGTGGCAATTGTTAG
	719	TGGTAACCTGGGTGCTGCAGGTTA	TTAACCTGCAAGCACCCAGGTTACC
15	720	TATCGGAGCCACCATTGCGATTGGG	TCCCAATGCGAATGGTGGCTCCGAT
	721	TGTGAACCTGGCTTGCCCCAGGATTA	TTAACCTGGGGCAAGCCAGTTCAC
	722	TAGGCGATAGCATGGTCCCATATGA	TTCATATGGGACCATGCTATGCCCT
	723	TAACGGTATCGTGGCTAATGCACGA	TTCGTGCATTAGCCACGATACCGTT
	724	TAGTAGTGGCCTCCAGATCGGCAA	TTTGCCTGATCTGGAGGACCACTACT
20	725	TCCGTTGAATTGGACGGGAGGTTAG	TCTAACCTCCCCTCCAATTCAACGG
	726	TGCATAAGTGGCATCGCGAAGGG	TCCCTTCGCGATGCCGACTTATGC
	727	TCGACAAGATGCAGCTGCTACATGC	TGCATGTAGCAGCTGCATCTTGTG
	728	TTCGCAGTGATTCCCACCGATAAG	TCTTATCGGTGGGAATCACTGCGA
	729	TCAAGGCGAGTCCACTCGAGGGGAC	TGTCCCCCTCGAGTGGACTCGCCTTG
25	730	TGCAACTTGCACGGCATAAGTGGCC	TGGCCACTTATGCCGTGCAAGTTGC
	731	TTCCGAGCTTGACGTTGCGACGTC	TGACGTCGCGAACGTCAAGCTCGGA
	732	TAGCGCTGGGCTGTGCTGCCATCTC	TGAGATGGCAGCACAGCCCAGCGCT
	733	TTTCATGTCGCTGAGTAACCTCGC	TGCGAGGGTTACTCAGCGACATGAA
	734	TCGAACCGCTAATGCCATTGTCAG	TCTGACAATGGCATTAGCGGTTCG
30	735	TCACGGAAGGTGGGACAAATCGCCG	TCCGGCATTGTCCCACCTTCCGTG
	736	TCACAGATGGAGACAAACGCGCCTT	TAAGGCGCGTTGTCTCCATCTGTG
	737	TTTTTCGCAACTCGCTCCATAACCC	TGGGTTATGGAGCGAGTTGCGAAAA
	738	TACGTTACGTTCCGGCGCTCTAA	TTTAGAGGCCGGAAACGTAACGT
	739	TTATCGGATTGCGTGGGTTCAATC	TGATTGAAACCCACGCAATCCGATA
35	740	TCTTCCACAATTGTCGCGACGCAC	TGTGCGTCGCGACAAATTGTTGAAAG
	741	TTGCACAAAGGTATGGCTGTCCGGC	TGCCGGACAGCCATACTTGTGCA
	742	TTCCGATGCCAGTCCCATCTTAAAGA	TTCTTAAGATGGGACTGGCATCGGA
	743	TCTGAAACCGTGCAGACGGACGCCA	TTCACCTCGATTGCGACGGTTTCAG
	744	TCGGTGTTCGGCGTGTGAAAAAAT	TATTTTTTCGACACGCCGGAAACACCG
40	745	TTCTAGCAGGCCTTTGAATGCCA	TTGGCGATTCAAAGGCCTGCTAGA
	746	TGAGTCACCTCTGAGACGGACGCCA	TTGGCGTCCGTCTCAGAGGTGACTC
	747	TTCTTCTGTCATCCTGAGCAGCAGCAT	TATGCTGTCAGGATGACAGAAGA
	748	TGCGGATGAAACCTGAAAGGGGCCT	TAGGCCCTTCAGGTTCATCCGC
	749	TGGGGCCCCAAACTGGTATCAAGCC	TGGCTTGATACCAAGTGGGGCCCC
	750	TGCATTGGCTCGGATTCTCCTACA	TTGTAGGAGAATCGAAGCCAATGC

	751	TAGGC GGCCC AACTGTGAGGTCTTG	TCAAGACCTCACAGTTGGGCCCT
5	752	TACACCATGTGCTCCCGCTGCAGT	TACTGCAGCGCGGAGCACATGGTGT
	753	TACGATGAACATGAATCGGGAGTCG	TCGACTCCCATTATGTTCATCGT
	754	TCTGCATCCCTGTAGCAGCGCTCCG	TCGGAGCGCTGCTACAGGGATGCAG
	755	TGTGCCGTATTCGACCTGTGCGTT	TAACGCACAGGTCGAAATACGGCAC
	756	TGCA GTGC GCACTTCAGTTAAAAG	TCTTTGA ACTGAAGTGC GCACTGC
	757	TGCGATTTAAGCGATGCCTGACG	TCGTCAAGGCATCGCTAAAATCGC
10	758	TTAGGTGACCTAGGCTTGCTTGCGG	TCCGCAAGCAAGCCTAGGTACCTA
	759	TCTGGATACCTTGCCTGTGCGGGCG	TGGCGCCGACAGGCAAGGTATCCAG
	760	TCCCCTTACGGCTCGTCGTCTATGC	TGCATAGACGACGAGGCCGTAAGGGG
	761	TGCGCTGCCGATGCGATGCATTA	TTAACATGCATCGCATGGCAAGCGC
	762	TTTCTGTAAGCGGCCCTGGGTTCA	TTGAACCCCAGGCCGTTACAGAAA
	763	TGGCTGAGGTGAGCGGTAAGGATGA	TTCATCCTTACCGCTCACCTCAGCC
	764	TTCTGGCCTCCCCGATCTAATTG	TCAAATTAGATGGGGAGGCCAAGA
15	765	TGGAGGTAAACGCCGTGACGTAGGA	TTCCCTACGTACACGGCGTTACCTCC
	766	TGTAATCCATTGTGGCTGCGTCAA	TTTGACGCA GCCACAAATGGATTAC
	767	TCAAACCCATTCCAGCAGACGCCTG	TCAGGCGTCTGCTGGAATGGTTTG
	768	TTAGGAGGAATTGGCATGCGGGCG	TCGCCCGCATGCCAATT CCTCCTA
	769	TATAGGTAGGATGTGCCCGGCGTTG	TCAACGCCGGGACATCCTACCTAT
20	770	TGCAAGTGCCTAGCTCGTCAGCCTC	TGAGGCTGACGAGCTAACGACTTGC
	771	TCTGGCTGTGCGATCTGTTAAC	TGTTAACGAGATGCGACACAGCCAG
	772	TCTAACGTGCTCGCGCAATCACT	TAGT GATTGCGCAGACGACGTTAG
	773	TTTTCATAAACGTTGCCCGAGC	TGCTGGGGACAACGTTATGAAAA
	774	TAGCAGGAGGACGAACCTCCGCTCC	TGGAGCGGAGGTTCGTCCTCCTGCT
25	775	TTTCAAGCACCATGTCGAATCAA	TTGGATTGACGATGGTGCTTGAA
	776	TAGCGTCGCCAGTGATCGCTAGTGG	TCCACTAGCGATCACTGGCAGCCT
	777	TTACATTCCCTGCCCTCCGTGGCCTT	TAAGCCCACGGAGGCAGGGAAATGTA
	778	TCGCTCGCGTATTCA GTAGCGGTT	TAACCGCTACTGAATACGCGAACG
	779	TTCGGACGCCGTCGACACTCATTATA	TTATAATGAGTGTGACGCCGTCCGA
30	780	TTCTGAGCAGGCCAGCGCTCCAGCT	TAGCTGGAGCGCTGGCCTGCTCAGA
	781	TTTGAATTGCCAAGCCCTGAAAGCC	TGGCTTCAGGGCTGGCAATTCAA
	782	TAGTTTCGCTTGATGCGTCGGTG	TCACCGACGCACTCAAGGCGAAACT
	783	TGTTTCATAGGCCACGCCGTGCTAAA	TTTAGCAGCGTGGCCTATGAAAC
	16	TCATCGCTGCAAGTACCGCACTCAA	TTTGAGTGC GGACTTGAGCGATG

CLAIMS

We claim:

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1. An oligonucleotide array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

10 2. An array according to claim 1, wherein said capture probes are microspheres.

3. An array according to claim 1 or 2 wherein said array is a liquid array.

4. An array according to claim 1, 2 or 3, wherein said array further comprises a solid support.

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5. An array according to claim 1, 2, 3 or 4, wherein said addresses are microspheres and wherein said solid support comprises wells into which said microspheres are individually distributed.

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6. An array according to claim 1, 2, 3 or 4, wherein each address is a different known location, and wherein each capture probe is attached to one of said known locations.

7. An array according to claim 1, 2, 3, 4, 5 or 6, wherein said array comprises at least 50 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

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8. An array according to claim 1, 2, 3, 4, 5 or 6 wherein said array comprises at least 100 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

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9. A kit comprising at least twenty-five nucleic acids selected from the group consisting of sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

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10. A kit according to claim 9, wherein said kit comprises at least 50 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

11. A kit according to claim 9 or 10, wherein said kit comprises at least 100 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.
- 5 12. A kit according to claim 9, 10 or 11, wherein said nucleic acids further comprise at least a first universal priming sequence.
- 10 13. A kit according to claim 9, 10, 11 or 12, wherein said nucleic acid sequence further comprises a sequence substantially complementary to a target domain.
- 15 14. A method of immobilizing a target nucleic acid sequence, said method comprising:
a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;
b) contacting said modified first target nucleic acid sequence with an array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4, whereby said target nucleic acid sequence is immobilized.
- 20 15. A method of detecting a target nucleic acid sequence, said method comprising:
a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;
b) contacting said modified first target nucleic acid sequence with an array comprising:
an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4; and
c) detecting the presence of said modified first target nucleic acid sequence.
- 25 16. A method of detecting a target nucleic acid, said method comprising:
a) hybridizing a first adapter probe with a first target nucleic acid, said first adapter probe comprising a first domain that is complementary to said first target nucleic acid and a second domain, said second domain comprising a first sequence substantially complementary to a selected from the group consisting of the sequences set forth in Table I, Table II, Table III and Table IV to form a first hybridization complex;

- b) contacting said first hybridization complex with an enzyme such that when said first domain of said adapter probe is perfectly complementary with said first target nucleic acid, said first adapter probe is altered resulting in a modified first adapter probe;
- c) contacting said modified first adapter probe with a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that said first capture probe and said modified first adapter probe form a second hybridization complex; and
- d) detecting the presence of said modified first adapter probe as an indication of the presence of said target nucleic acid.

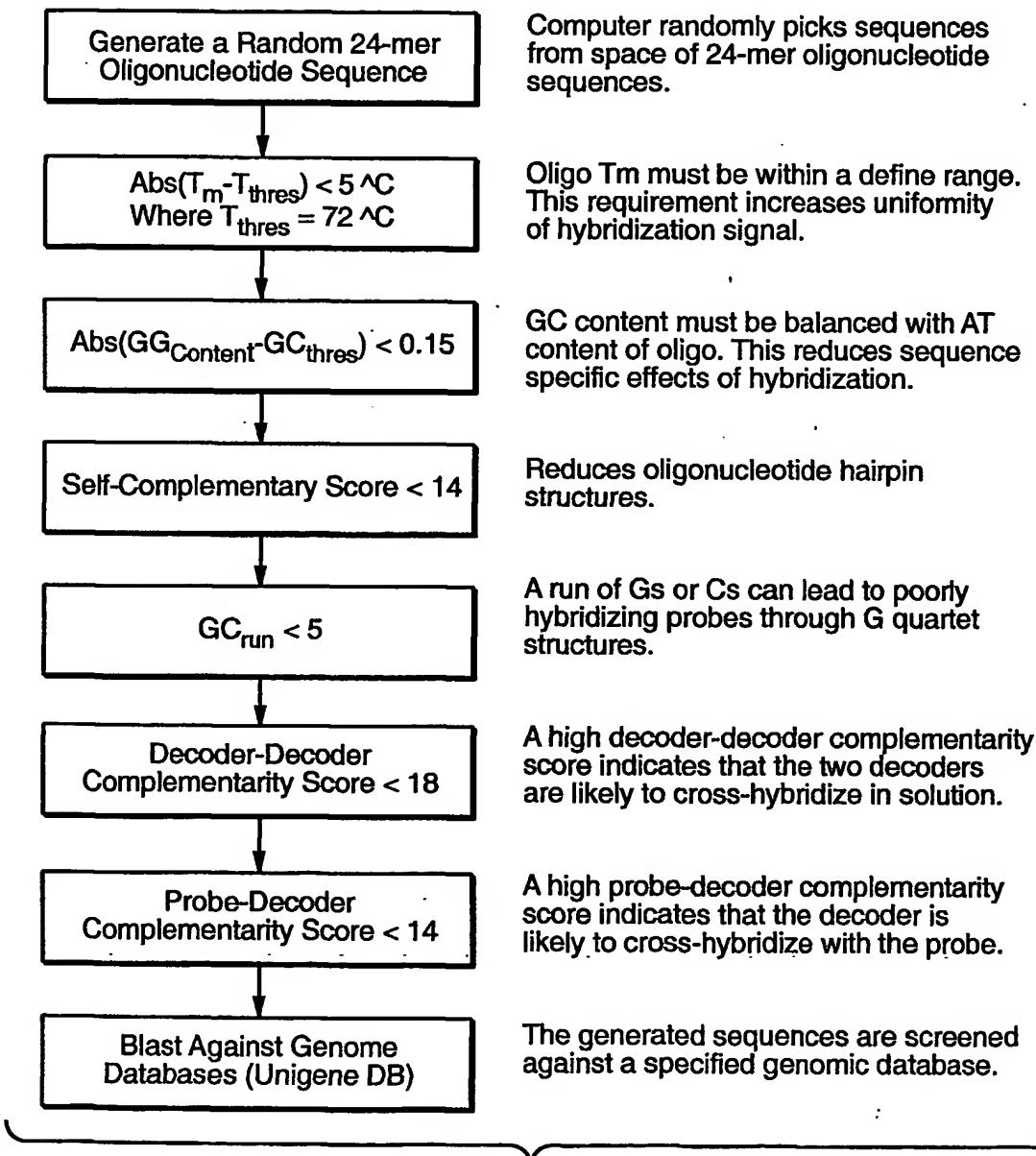
5

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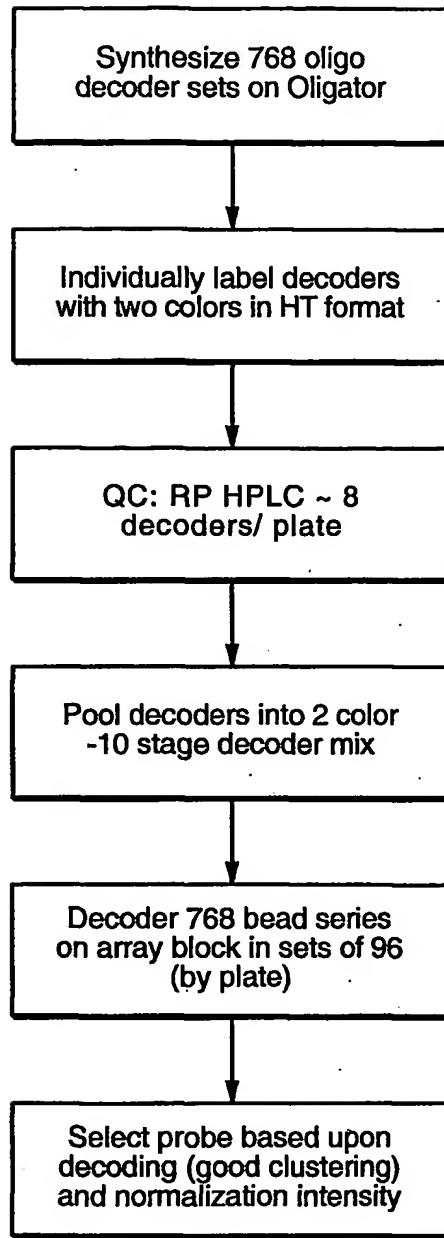
Description of algorithm to select “best” oligonucleotide adapter sequences.**Requirements for good sequences:**

- Generates adequate hybridization signal intensity when employed in an experiment.
- Exhibits minimal cross-reactivity with other adapter sequences.
- Unique within the human genome sequence. This requirement can be extended to the genomic sequence of other organisms such as the fruit fly, the mouse, etc.

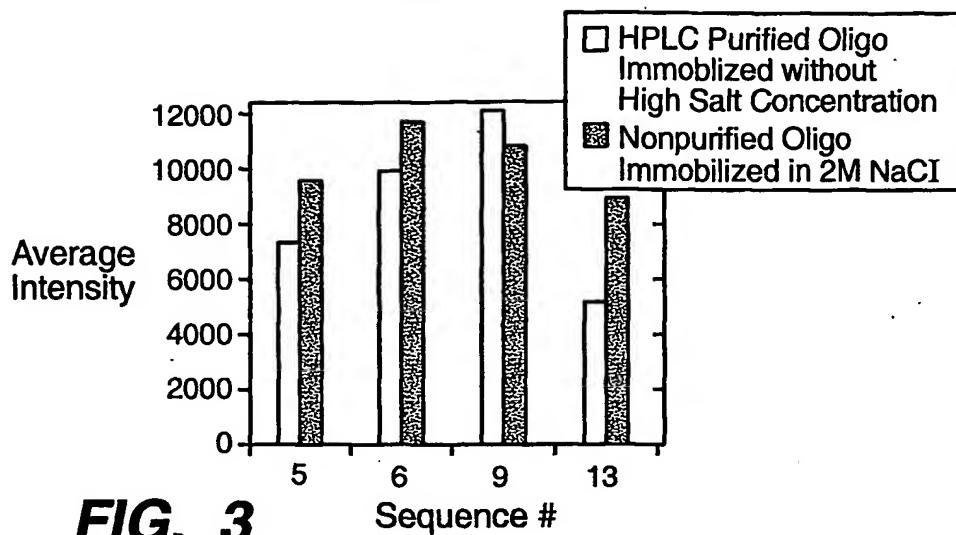
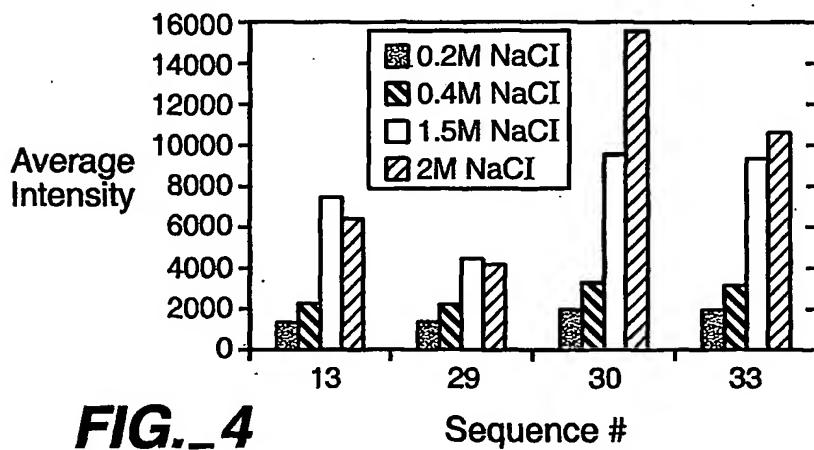
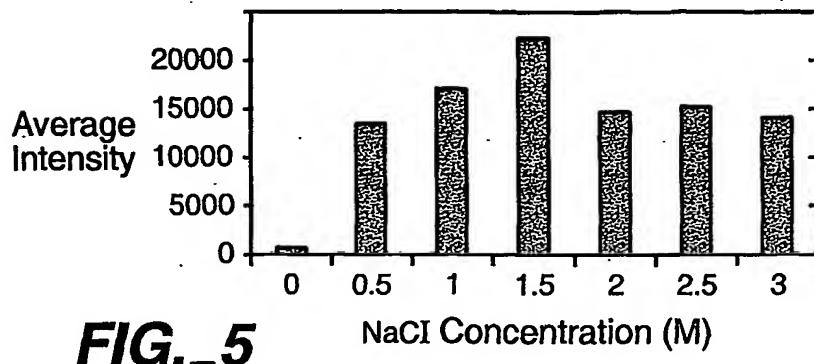
One method of generating sequences that meet the above requirements is to randomly generate sequences of given lengths and then pass these filters through a set of heuristic acceptance filters. In particular, the 24-mer Illumina Adapter sequences (IllumaCodes) were chosen as follows.

**FIG._1**

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**Flow diagram for selection
of probes sequences****FIG._2**

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**FIG.-3****FIG.-4****FIG.-5**